

cct gcc gat ggt ttc gag cgt gcc gtt gat ctt tca caa gga cgt gtg 595  
 Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu Ser Gln Gly Arg Val  
 150 155 160 165  
 gtg atc aat ctg gct cca gtt gtg ccc gtg gga cat gat cag ctg cgt 643  
 Val Ile Asn Leu Ala Pro Val Val Pro Val Gly His Asp Gln Leu Arg  
 170 175 180  
 cgt gcc gat cca ttg ctg gtc aac gaa cac gaa ggc gct ctg gtg ctg 691  
 Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu Gly Ala Leu Val Leu  
 185 190 195  
 gac atg ctt gga act cca gcg acc acg tct gat ccc caa agt ttg gtc 739  
 Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp Pro Gln Ser Leu Val  
 200 205 210  
 act gaa ttg ctg gag cag ggt ttt act tcc gtg gtg atg aca ctt ggt 787  
 Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val Val Met Thr Leu Gly  
 215 220 225  
 gcc gaa ggt gct ctg gtt ggc acg ccg ggc caa ctc acg gca att cct 835  
 Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln Leu Thr Ala Ile Pro  
 230 235 240 245  
 acc cca aag 844  
 Thr Pro Lys

<210> 390  
 <211> 248  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 390  
 Met Asp Ser Pro Met Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val  
 1 5 10 15  
 Gly Ser Ile Asn Ala Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu  
 20 25 30  
 Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly  
 35 40 45  
 Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val  
 50 55 60  
 Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu  
 65 70 75 80  
 Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val  
 85 90 95  
 Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu  
 100 105 110  
 Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu  
 115 120 125  
 Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu

130 135 140

Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu  
 145 150 155 160

Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly  
 165 170 175

His Asp Gln Leu Arg Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu  
 180 185 190

Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp  
 195 200 205

Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val  
 210 215 220

Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln  
 225 230 235 240

Leu Thr Ala Ile Pro Thr Pro Lys  
 245

<210> 391  
 <211> 1026  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1003)  
 <223> RXA02797

<400> 391  
 acagtctcat gaagccataa taaccacctt ctacaaagat cgacgtagaa tggaataacc 60

cottatgaaa acgtttgcat aactccgcta aggatgttcc atg aat aat cga att 115  
 Met Asn Asn Arg Ile  
 1 5

gtc gta gtc ggc tcc atc aac gct gat ctt aat gtt ctc gtt gac cgc 163  
 Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg  
 10 15 20

cac cca gca cct ggc gaa aca ctg ttg ggc agt ggt gga cac atc act 211  
 His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr  
 25 30 35

gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt 259  
 Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Leu Gln Gly  
 40 45 50

gca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc 307  
 Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala  
 55 60 65

cca gcc tta gaa ttc ctt cgt tcg tca ggc gtc gac ctt acg gca gta 355  
 Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val Asp Leu Thr Ala Val  
 70 75 80 85



tcc gaa gta gat gac acc acc ggg ctt gca gtt atc acc gtt gcc aaa	403
Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val Ile Thr Val Ala Lys	
90 95 100	
gac ggc gag aac aat atc gtt gtc atc ccc ggc gcg aat tcc ctg gtc	451
Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly Ala Asn Ser Leu Val	
105 110 115	
aat tgt gat tat gta agc agc caa tcc gct ctt tta gct gaa gct gga	499
Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu Leu Ala Glu Ala Gly	
120 125 130	
atc ctg ttg ctg caa ggt gag atc cct gcg gat ggc ttc aaa gag gcc	547
Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Lys Glu Ala	
135 140 145	
att cac cac acc atg ggt cgc gtc gtg gtg aat cta gcg ccc gtc atc	595
Ile His His Thr Met Gly Arg Val Val Val Asn Leu Ala Pro Val Ile	
150 155 160 165	
gag gta gag aag tcc gcg tta ctt gag gct gat ccg atc atc gcc aat	643
Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp Pro Ile Ile Ala Asn	
170 175 180	
gag cac gag gcc ggc ctg att ctg gat caa ttc ggg gca ggc atc gat	691
Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe Gly Ala Gly Ile Asp	
185 190 195	
tcc atg gat ccc cac gag ctc gcg caa gct ctc ctc gac gcc ggt ttc	739
Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu Leu Asp Ala Gly Phe	
200 205 210	
gcc tct gtt gtt tta acg ctt gga tcc gca ggc gcg ttg gtc gcc gat	787
Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly Ala Leu Val Ala Asp	
215 220 225	
gcc acc ggt atc acg gac atc gcc aca cca acg gtg cag gca gtt gac	835
Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr Val Gln Ala Val Asp	
230 235 240 245	
acc acg gga gcc ggt gac gct ttt gcc gga gcc ttc tgc gca cga cta	883
Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala Phe Cys Ala Arg Leu	
250 255 260	
att aaa ggc gat tcg ctt atc gac gcc gcc acc cac gca gca cgc gtc	931
Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr His Ala Ala Arg Val	
265 270 275	
ggc gct tac tcg gtg caa acc gcc gga gcg caa gcg tcc tat ccg gac	979
Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln Ala Ser Tyr Pro Asp	
280 285 290	
gcg agc gtt tca ctt ccc tct gtt taaaaaaaaact atttaagaag agg	1026
Ala Ser Val Ser Leu Pro Ser Val	
295 300	

&lt;210&gt; 392

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 392

Met Asn Asn Arg Ile Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn  
 1 5 10 15  
 Val Leu Val Asp Arg His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser  
 20 25 30  
 Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala  
 35 40 45  
 Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys  
 50 55 60  
 Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val  
 65 70 75 80  
 Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val  
 85 90 95  
 Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly  
 100 105 110  
 Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu  
 115 120 125  
 Leu Ala Glu Ala Gly Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp  
 130 135 140  
 Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn  
 145 150 155 160  
 Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp  
 165 170 175  
 Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe  
 180 185 190  
 Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu  
 195 200 205  
 Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly  
 210 215 220  
 Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr  
 225 230 235 240  
 Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala  
 245 250 255  
 Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr  
 260 265 270  
 His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln  
 275 280 285  
 Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val  
 290 295 300

&lt;210&gt; 393

<400> 393																	
ccaacatcgc	cttgcacgta	ataggttaaa	acacaagtga	atgtaatcgt	ttgcagcaat	60											
cgattacata aaggtagata atgagataaa gcgaggcgct						atg	gcg	acg	gaa	aaa	115						
						Met	Ala	Thr	Glu	Lys							
						1				5							
ttc	cga	ccg	act	ctt	aaa	gat	gtc	gct	cgt	caa	gca	ggt	gtc	tcc	atc	163	
Phe	Arg	Pro	Thr	Leu	Lys	Asp	Val	Ala	Arg	Gln	Ala	Gly	Val	Ser	Ile		
				10				15					20				
gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg						211											
Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser																	
						25			30				35				
act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc						259											
Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala																	
						40			45				50				
aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt						307											
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly																	
						55			60				65				
gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act						355											
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr																	
						70			75				80			85	
gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc						403											
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr																	
						90			95				100				
aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc						451											
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu																	
						105			110				115				
acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc						499											
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys																	
						120			125				130				
gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg						547											
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu																	
						135			140				145				
gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct						595											
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser																	
						150			155				160			165	
aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac						643											
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn																	
						170			175				180				
aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca						691											

```

Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr
      185                      190                      195

ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa 739
Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys
      200                      205                      210

att ggc gaa cag ctc gtt ttt ctg ggt ggg tac gaa caa agc gtt gga 787
Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr Glu Gln Ser Val Gly
      215                      220                      225

ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt 835
Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe
      230                      235                      240

gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag 883
Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys
      250                      255                      260

gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca 931
Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr
      265                      270                      275

cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa 979
His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln
      280                      285                      290

aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta 1027
Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu
      295                      300                      305

att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc 1075
Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala
      310                      315                      320                      325

ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat 1123
Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp
      330                      335                      340

gga ctc ccc aat gag taactcaacc ggtaccgaca ttg 1161
Gly Leu Pro Asn Glu
      345

```

&lt;210&gt; 394

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 394

```

Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln
  1                      5                      10                      15

Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro
      20                      25                      30

Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp
      35                      40                      45

Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg
      50                      55                      60

```

Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe  
 65 70 75 80  
 Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu  
 85 90 95  
 Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly  
 100 105 110  
 Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val  
 115 120 125  
 Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly  
 130 135 140  
 Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile  
 145 150 155 160  
 Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu  
 165 170 175  
 Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro  
 180 185 190  
 Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala  
 195 200 205  
 Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr  
 210 215 220  
 Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly  
 225 230 235 240  
 Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile  
 245 250 255  
 Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val  
 260 265 270  
 Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu  
 275 280 285  
 Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser  
 290 295 300  
 Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr  
 305 310 315 320  
 Thr Ile Pro Thr Ala Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr  
 325 330 335  
 Leu Arg Lys Lys Asp Gly Leu Pro Asn Glu  
 340 345

&lt;210&gt; 395

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(460)

&lt;223&gt; RXA02551

&lt;400&gt; 395

gctgcacaaa ttccgcgaaa gggatcacc atcgacatca cagatgaaga ccgtgagatc 60

ttaaaaaac accgtcgatt tcatttcctt ctcctattac atg tcc gta tgt gaa 115  
Met Ser Val Cys Glu  
1 5

gcc cac aac ccc gaa aac tac tca acc ggt ggc ggt aac atc atc ggc 163  
Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly Gly Asn Ile Ile Gly  
10 15 20

gga gtg gtc agc ccc act ctc gcg gct tcc gaa tgg ggt tgg caa gtt 211  
Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu Trp Gly Trp Gln Val  
25 30 35

gat ccc ctc ggt ttg cgc atc gtc ctg aac aac tac tgg gag cgc tgg 259  
Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn Tyr Trp Glu Arg Trp  
40 45 50

cag aag cca ctg ttc atc gtc gaa aac gga cta gga gca aag gac gtg 307  
Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val  
55 60 65

ctt atc gac gga ccc tcc ggc cca aca gta aac gat gac tac cgc atc 355  
Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile  
70 75 80 85

aaa tac ctc gac gac ggc ggc tca gga atc ttg aag cgc tac aag aag 403  
Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys  
90 95 100

aag tcc ttt gat tgg tgc cgc gac atc atc gcc acc aat ggc gaa agc 451  
Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala Thr Asn Gly Glu Ser  
105 110 115

ctg gaa tcc taagaaataa aggtagggtg cac 483  
Leu Glu Ser  
120

&lt;210&gt; 396

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 396

Met Ser Val Cys Glu Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly  
1 5 10 15

Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu  
20 25 30

Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn  
35 40 45

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu

50	55	60
Gly Ala Lys Asp Val Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn		
65	70	75
Asp Asp Tyr Arg Ile Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu		
85	90	95
Lys Arg Tyr Lys Lys Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala		
100	105	110
Thr Asn Gly Glu Ser Leu Glu Ser		
115	120	

<210> 397  
 <211> 795  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(772)  
 <223> RXA01325

<400> 397  
 gcgcagcgct cggacgatta cgaacttcag gagaactcgg ggtcattcgt tgcattctac 60  
 cctggaaatt ttccacact aagtcaggtc taagtagggt atg gat atg acg att 115  
 Met Asp Met Thr Ile  
 1 5  
 tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca 163  
 Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro  
 10 15 20  
 gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag 211  
 Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu  
 25 30 35  
 ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act 259  
 Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr  
 40 45 50  
 gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc 307  
 Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe  
 55 60 65  
 ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt 355  
 Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu  
 70 75 80 85  
 gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg 403  
 Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Val Leu Asp Ile Ala  
 90 95 100  
 gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca 451  
 Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu Gln Glu Ile Val Ala  
 105 110 115  
 atc agg gag gct gtt cca tct cct gtg gtg ctg aaa ttc atc ctc gaa 499

Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu Lys Phe Ile Leu Glu  
 120 125 130

aca gct gtt gtg agt gat gaa gca att gtg act gca gtg aat gcg ttg 547  
 Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr Ala Val Asn Ala Leu  
 135 140 145

att gct gct ggt gct gac ttc gct aaa act tcc acg gga ttc cac cca 595  
 Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser Thr Gly Phe His Pro  
 150 155 160 165

gcg gga ggg gca act gtt gag gct gtt cgg gtg atg gct tgc gct tct 643  
 Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val Met Ala Ser Ala Ser  
 170 175 180

cgg gga agg gtt gga att aag gct gcc ggt ggg gtg aaa act tgg gaa 691  
 Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly Val Lys Thr Trp Glu  
 185 190 195

gat gcg gtg gcg ttt gtt gaa gca ggg gct act cgc att gga act tct 739  
 Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser  
 200 205 210

aat gcg gga gcc att ttg gag ggt gcg ccg gag tagtttggcg ttctaatacgg 792  
 Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu  
 215 220

gac 795

&lt;210&gt; 398

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 398

Met Asp Met Thr Ile Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr  
 1 5 10 15

Thr Leu Leu Gly Pro Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile  
 20 25 30

Asp Ser Ala Ile Glu Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser  
 35 40 45

Met Val Asn Leu Thr Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala  
 50 55 60

Thr Val Ala Gly Phe Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala  
 65 70 75 80

Ala Glu Ala Arg Leu Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val  
 85 90 95

Val Leu Asp Ile Ala Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu  
 100 105 110

Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu  
 115 120 125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr



130	135	140
Ala Val Asn Ala Leu Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser		
145	150	155
Thr Gly Phe His Pro Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val		
	165	170
Met Ala Ser Ala Ser Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly		
	180	185
Val Lys Thr Trp Glu Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr		
	195	200
Arg Ile Gly Thr Ser Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu		
	210	220

<210> 399  
 <211> 684  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(661)  
 <223> RXA00195

<400> 399  
 tcgcagtcacat catgcaggca taacctgaaa cccatccggtt tggattgccc caaatgggtg 60  
 tagtgggtgc gtttacccaa caagtgaag aatgggagtc gtg act aaa aag atc .115  
 Val Thr Lys Lys Ile  
 1 5  
 ctt att ttg gga agc act ggt tcg att gga act cag gcg ctg gac gtt 163  
 Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr Gln Ala Leu Asp Val  
 10 15 20  
 att gct gat aat tca gac aag ttt gag gtg gtg ggt atc gct gcg ggc 211  
 Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val Gly Ile Ala Ala Gly  
 25 30 35  
 ggt tct cag cca gac ctc gtt att tcg cag gcg cag cag ttg ggg ctg 259  
 Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala Gln Gln Leu Gly Leu  
 40 45 50  
 gct gca gac aag gtt gcg gtt gct gat gca cag gct gcc gca gta att 307  
 Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln Ala Ala Ala Val Ile  
 55 60 65  
 tcg aag gct ctc ggc ggc gag atc atc tct gga acc gat gct gcg aag 355  
 Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly Thr Asp Ala Ala Lys  
 70 75 80 85  
 att ctg gtg gaa acc aca aag gcc gac act gtg ctt aat gct ctg gtt 403  
 Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val Leu Asn Ala Leu Val  
 90 95 100

ggt tct ttg ggg ctt gcg gca acg ctg gcc act ctg gaa tct ggt gcg 451  
 Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr Leu Glu Ser Gly Ala  
 105 110 115  
 cat ctt gcc ttg gct aac aaa gaa tcg ctg gtt gcc ggt ggt gag ttt 499  
 His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val Ala Gly Gly Glu Phe  
 120 125 130  
 gtt acc tca aag gca aag ctg ggg cag atc att ccg gtc gat tcg gag 547  
 Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile Pro Val Asp Ser Glu  
 135 140 145  
 cac tct gcc atg gcg cag tgt ttg cgt tcg ggt act cgt gat gag gtt 595  
 His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly Thr Arg Asp Glu Val  
 150 155 160 165  
 gcg cgg att gtg ctg aca gct tcg ggc gga cct ttc agg gct gga cca 643  
 Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro Phe Arg Ala Gly Pro  
 170 175 180  
 ggg aga aga tgt ggg agg tgactcccga gcaggcagca gcg 684  
 Gly Arg Arg Cys Gly Arg  
 185

&lt;210&gt; 400

&lt;211&gt; 187

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 400

Val Thr Lys Lys Ile Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr  
 1 5 10 15  
 Gln Ala Leu Asp Val Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val  
 20 25 30  
 Gly Ile Ala Ala Gly Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala  
 35 40 45  
 Gln Gln Leu Gly Leu Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln  
 50 55 60  
 Ala Ala Ala Val Ile Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly  
 65 70 75 80  
 Thr Asp Ala Ala Lys Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val  
 85 90 95  
 Leu Asn Ala Leu Val Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr  
 100 105 110  
 Leu Glu Ser Gly Ala His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val  
 115 120 125  
 Ala Gly Gly Glu Phe Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile  
 130 135 140  
 Pro Val Asp Ser Glu His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly  
 145 150 155 160

Thr Arg Asp Glu Val Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro  
 165 170 175

Phe Arg Ala Gly Pro Gly Arg Arg Cys Gly Arg  
 180 185

<210> 401  
 <211> 738  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(715)  
 <223> RXA00196

<400> 401  
 ctgccatggc gcagtggttg cggttcgggta ctcgatgatga ggttgcgcg attgtgctga 60

cagcttcggg cggacctttc agggctggac cagggagaag atg tgg gag gtg act 115  
 Met Trp Glu Val Thr  
 1 5

ccc gag cag gca gca gcg cac cca acg tgg gcg atg ggg cag atg aac 163  
 Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala Met Gly Gln Met Asn  
 10 15 20

acg ttg aac tcc gcc acc ctt att aat aaa ggc ctc gaa ctc atc gag 211  
 Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly Leu Glu Leu Ile Glu  
 25 30 35

gcg acc ctg ctg ttt gaa acg gat gcg gat ctc att gat gtg acg gtg 259  
 Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu Ile Asp Val Thr Val  
 40 45 50

cat ccg cag tcg atc atc cac tcc atg atc acg ttt acg gat ggt gcg 307  
 His Pro Gln Ser Ile Ile His Ser Met Ile Thr Phe Thr Asp Gly Ala  
 55 60 65

acc atc gcg cag gcg tcg cca cca tcg atg aaa ctg ccg atc gcg ttg 355  
 Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys Leu Pro Ile Ala Leu  
 70 75 80 85

gcg ctt gat tgg cca cat cgg gtg ccg aag gct cag ccg gcg ctg gat 403  
 Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala Gln Pro Ala Leu Asp  
 90 95 100

ttc acc gct gct cat acc tgg gct ttt gag ccg gtg gat gat gcc gca 451  
 Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro Val Asp Asp Ala Ala  
 105 110 115

ttc cct gcg gtg cag ctg gct agg cac gtc gca aag caa aaa ggc acg 499  
 Phe Pro Ala Val Gln Leu Ala Arg His Val Ala Lys Gln Lys Gly Thr  
 120 125 130

tac ccc gcg gtg tat aac gcc gcc aac gag gag gcg gct gag gcg ttt 547  
 Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu Ala Ala Glu Ala Phe  
 135 140 145

ttg cgc ggg cga atc aag ttt ccg cag atc gtg gac gtg gtg gac gag 595  
 Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val Asp Val Val Asp Glu  
 150 155 160 165  
  
 gtc ctc caa gga gct tct cag ttt gct ggt gta gca tca cac gtc gat 643  
 Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val Ala Ser His Val Asp  
 170 175 180  
  
 gat att ttg gca acc gaa tct gag gca cgc gcg cgt gcg aat gct ttg 691  
 Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala Arg Ala Asn Ala Leu  
 185 190 195  
  
 atc aac cgg ttg gca acc aac ttg taagctaagg agcttccgcc tcg 738  
 Ile Asn Arg Leu Ala Thr Asn Leu  
 200 205

&lt;210&gt; 402

&lt;211&gt; 205

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 402

Met Trp Glu Val Thr Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala  
 1 5 10 15  
 Met Gly Gln Met Asn Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly  
 20 25 30  
 Leu Glu Leu Ile Glu Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu  
 35 40 45  
 Ile Asp Val Thr Val His Pro Gln Ser Ile Ile His Ser Met Ile Thr  
 50 55 60  
 Phe Thr Asp Gly Ala Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys  
 65 70 75 80  
 Leu Pro Ile Ala Leu Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala  
 85 90 95  
 Gln Pro Ala Leu Asp Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro  
 100 105 110  
 Val Asp Asp Ala Ala Phe Pro Ala Val Gln Leu Ala Arg His Val Ala  
 115 120 125  
 Lys Gln Lys Gly Thr Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu  
 130 135 140  
 Ala Ala Glu Ala Phe Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val  
 145 150 155 160  
 Asp Val Val Asp Glu Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val  
 165 170 175  
 Ala Ser His Val Asp Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala  
 180 185 190  
 Arg Ala Asn Ala Leu Ile Asn Arg Leu Ala Thr Asn Leu  
 195 200 205

<210> 403  
 <211> 2031  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2008)  
 <223> RXN01562

<400> 403  
 gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtaaa 60  
 ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac 115  
 Met Gly Ile Leu Asn  
 1 5  
 agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163  
 Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu  
 10 15 20  
 gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211  
 Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala  
 25 30 35  
 gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259  
 Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr  
 40 45 50  
 atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307  
 Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe  
 55 60 65  
 gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355  
 Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala  
 70 75 80 85  
 aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403  
 Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr  
 90 95 100  
 tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg 451  
 Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser  
 105 110 115  
 gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499  
 Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp  
 120 125 130  
 ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547  
 Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu  
 135 140 145  
 act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595  
 Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys  
 150 155 160 165  
 gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643  
 Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser

170	175	180	
cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag			691
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln			
185	190	195	
cct ttc tat gat cgc ttc atg gaa aag ggc aag acg tcc ctg aaa tcc			739
Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys Thr Ser Leu Lys Ser			
200	205	210	
atg ggg tgg gta ggg gag cgt act ttt gaa gcg ctc cat gca ttt aaa			787
Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala Leu His Ala Phe Lys			
215	220	225	
gaa ggt gtg aag agc acc gtc att ccc acc gaa atg ttc cct gaa ctg			835
Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu Met Phe Pro Glu Leu			
230	235	240	245
ggc atg aaa tac gtg ggt ccg gtt gat gga cat aac caa aaa gct gtc			883
Gly Met Lys Tyr Val Gly Pro Val Asp Gly His Asn Gln Lys Ala Val			
250	255	260	
gac aat gcg ctg aaa tac gct cat gat tat gat ggc ccc atc atc gtg			931
Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp Gly Pro Ile Ile Val			
265	270	275	
cac atg gtc acc gaa aag ggt cgt ggt tac gcg cct gct gag cag gat			979
His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala Pro Ala Glu Gln Asp			
280	285	290	
ttg gac gaa ttg atg cac tcc acg ggc gtc atc gat ccg ctc aca gga			1027
Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro Leu Thr Gly			
295	300	305	
gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg ttc agc gat			1075
Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val Phe Ser Asp			
310	315	320	325
gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt gcc atc acc			1123
Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val Ala Ile Thr			
330	335	340	
gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa gcc aat ttc			1171
Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu Ala Asn Phe			
345	350	355	
ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac gcg gta act			1219
Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His Ala Val Thr			
360	365	370	
tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg gtg gct att			1267
Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val Val Ala Ile			
375	380	385	
tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc atg gat gtg			1315
Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu Met Asp Val			
390	395	400	405
ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc tca ggt gtc			1363
Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg Ser Gly Val			
410	415	420	

acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat atg gcg ctg	1411
Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp Met Ala Leu	
425 430 435	
acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt gat gag gat	1459
Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg Asp Glu Asp	
440 445 450	
tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat gat ggc ccc	1507
Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp Asp Gly Pro	
455 460 465	
aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca att gtt gct	1555
Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro Ile Val Ala	
470 475 480 485	
atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat gaa gac gcc	1603
Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr Glu Asp Ala	
490 495 500	
act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc atc att gcg	1651
Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu Ile Ile Ala	
505 510 515	
gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc agg att aaa	1699
Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser Arg Ile Lys	
520 525 530	
cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg att gtc ccc	1747
Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp Ile Val Pro	
535 540 545	
atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac ctc gtg atc	1795
Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp Leu Val Ile	
550 555 560 565	
acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc ttg ctc tct	1843
Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser Leu Leu Ser	
570 575 580	
gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga caa atc gcc	1891
Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg Gln Ile Ala	
585 590 595	
gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa gtg ctc gcc	1939
Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu Val Leu Ala	
600 605 610	
gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt gtt gga tgg	1987
Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val Val Gly Trp	
615 620 625	
ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg ccg	2031
Leu Asp Ser Leu Phe Gly Glu	
630 635	

&lt;210&gt; 404

&lt;211&gt; 636

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 404

Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu  
 1 5 10 15  
 Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu  
 20 25 30  
 Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly  
 35 40 45  
 Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln  
 50 55 60  
 Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile  
 65 70 75 80  
 Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly  
 85 90 95  
 Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu  
 100 105 110  
 Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys  
 115 120 125  
 Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val  
 130 135 140  
 Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn  
 145 150 155 160  
 Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Asn Asp Asn  
 165 170 175  
 Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala  
 180 185 190  
 Gly Leu Arg Met Gln Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys  
 195 200 205  
 Thr Ser Leu Lys Ser Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala  
 210 215 220  
 Leu His Ala Phe Lys Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu  
 225 230 235 240  
 Met Phe Pro Glu Leu Gly Met Lys Tyr Val Gly Pro Val Asp Gly His  
 245 250 255  
 Asn Gln Lys Ala Val Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp  
 260 265 270  
 Gly Pro Ile Ile Val His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala  
 275 280 285  
 Pro Ala Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile  
 290 295 300  
 Asp Pro Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr



305		310		315		320
Ser Val Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn	325		330		335	
Val Val Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys	340		345		350	
Phe Glu Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu	355		360		365	
Gln His Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His	370		375		380	
Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln	385		390		395	400
Leu Leu Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu	405		410		415	
Asp Arg Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val	420		425		430	
Trp Asp Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala	435		440		445	
Pro Arg Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser	450		455		460	
Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro	465		470		475	480
Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu	485		490		495	
Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser	500		505		510	
Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val	515		520		525	
Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro	530		535		540	
Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp	545		550		555	560
His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val	565		570		575	
Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro	580		585		590	
Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg	595		600		605	
Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr	610		615		620	
Thr Val Val Gly Trp Leu Asp Ser Leu Phe Gly Glu	625		630		635	

<210> 405  
 <211> 1061  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1038)  
 <223> FRXA01562

<400> 405  
 gag cag gat ttg gac gaa ttg atg cac tcc acg ggc gtc atc gat ccg 48  
 Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro  
 1 5 10 15  
 ctc aca gga gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg 96  
 Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val  
 20 25 30  
 ttc agc gat gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt 144  
 Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val  
 35 40 45  
 gcc atc acc gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa 192  
 Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu  
 50 55 60  
 gcc aat ttc ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac 240  
 Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His  
 65 70 75 80  
 gcg gta act tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg 288  
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val  
 85 90 95  
 gtg gct att tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc 336  
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu  
 100 105 110  
 atg gat gtg ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc 384  
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg  
 115 120 125  
 tca ggt gtc acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat 432  
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp  
 130 135 140  
 atg gcg ctg acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt 480  
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg  
 145 150 155 160  
 gat gag gat tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat 528  
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp  
 165 170 175  
 gat ggc ccc aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca 576  
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro  
 180 185 190

att gtt gct atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat 624  
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr  
 195 200 205  
  
 gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc 672  
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu  
 210 215 220  
  
 atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc 720  
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser  
 225 230 235 240  
  
 agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg 768  
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp  
 245 250 255  
  
 att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac 816  
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp  
 260 265 270  
  
 ctc gtg atc acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc 864  
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser  
 275 280 285  
  
 ttg ctc tct gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga 912  
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg  
 290 295 300  
  
 caa atc gcc gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa 960  
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu  
 305 310 315 320  
  
 gtg ctc gcc gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt 1008  
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val  
 325 330 335  
  
 gtt gga tgg ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg 1058  
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu  
 340 345  
  
 ccg 1061

&lt;210&gt; 406

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 406

Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro  
 1 5 10 15

Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val  
 20 25 30

Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val  
 35 40 45

Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu  
 50 55 60

Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His  
 65 70 75 80  
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val  
 85 90 95  
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu  
 100 105 110  
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg  
 115 120 125  
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp  
 130 135 140  
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg  
 145 150 155 160  
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp  
 165 170 175  
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro  
 180 185 190  
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr  
 195 200 205  
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu  
 210 215 220  
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser  
 225 230 235 240  
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp  
 245 250 255  
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp  
 260 265 270  
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser  
 275 280 285  
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg  
 290 295 300  
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu  
 305 310 315 320  
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val  
 325 330 335  
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu  
 340 345

&lt;210&gt; 407

&lt;211&gt; 703

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

<221> CDS  
 <222> (101)..(703)  
 <223> FRXA01705

<400> 407

```
gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtacaa 60
ccgtccgcat ccgagaagca aaggtgtctg actcgcgcga atg gga att ctg aac 115
                                     Met Gly Ile Leu Asn
                                     1 5
agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163
Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
                                     10 15 20
gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211
Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
                                     25 30 35
gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259
Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr
                                     40 45 50
atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe
                                     55 60 65
gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala
                                     70 75 80 85
aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr
                                     90 95 100
tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg 451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser
                                     105 110 115
gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp
                                     120 125 130
ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu
                                     135 140 145
act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys
                                     150 155 160 165
gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser
                                     170 175 180
cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln
                                     185 190 195
cct ttc tat gat 703
Pro Phe Tyr Asp
```

200

<210> 408  
 <211> 201  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 408  
 Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu  
 1 5 10 15  
 Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu  
 20 25 30  
 Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly  
 35 40 45  
 Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln  
 50 55 60  
 Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile  
 65 70 75 80  
 Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly  
 85 90 95  
 Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu  
 100 105 110  
 Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys  
 115 120 125  
 Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val  
 130 135 140  
 Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn  
 145 150 155 160  
 Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn  
 165 170 175  
 Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala  
 180 185 190  
 Gly Leu Arg Met Gln Pro Phe Tyr Asp  
 195 200

<210> 409  
 <211> 2241  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2218)  
 <223> RXN00879

<400> 409  
 caccocaaag cccaatccaa aagatgtatt ttctaacaaa cttaccctca cgctacaaat 60

atgctgtgcc cacacgctat tagtggcata atgttgtgtt	gtg act gct cgc aga	115
	Val Thr Ala Arg Arg	5
	1	
ttt ttg aat gaa ctc gcc gat ctc tac ggc gta gca act tcc tac act		163
Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr		20
	10 15	
gat tac aaa ggt gcc cat att gag gtc agc gat gac aca tta gtg aaa		211
Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys		35
	25 30	
atc ctg cgt gct ctg ggt gtg aat tta gat aca agc aac ctc ccc aac		259
Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn		50
	40 45	
gat gac gct atc caa cgc caa att gcc ctc ttc cat gat cga gag ttc		307
Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe		65
	55 60	
act cgc cca ctg cct cca tcg gtg gtt gca gtt gaa ggt gat gaa cta		355
Thr Arg Pro Leu Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu		85
	70 75 80	
gtt ttc ccg gtg cat gtg cac gac ggt tcc cct gca gat gtc cac atc		403
Val Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile		100
	90 95	
gaa ttg gaa gac ggc acg cag cgg gat gtt tct cag gtg gaa aac tgg		451
Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp		115
	105 110	
aca gcg cca cgg gaa att gat ggg att agg tgg ggc gag gca tcg ttt		499
Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe		130
	120 125	
aag att cct ggt gat ctc ccc ttg ggt tgg cac aag ctt cac ctt aaa		547
Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys		145
	135 140	
tcc aat gaa cgc tca gct gag tgc ggt ttg atc atc acc ccg gct cgt		595
Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg		165
	150 155 160	
ctg tct act gct gat aag tat ctt gat tcc cct cgc agt ggt gtc atg		643
Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met		180
	170 175	
gcg cag atc tac tct gtg cgt tcc acg ttg tcg tgg ggc atg ggt gat		691
Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp		195
	185 190	
ttc aat gat tta gga aac ttg gca agt gtg gtt gcc cag gat gga gca		739
Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala		210
	200 205 210	
gac ttc ctg ctc atc aac ccc atg cac gct gca gag ccg ctg cct cct		787
Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro		225
	215 220	

act gag gac tct cct tat ctg ccc aca acc agg cgc ttt atc aac ccg	835
Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro	
230 235 240 245	
atc tac att cgg gta gaa gat att ccg gag ttt aat cag ctt gag att	883
Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile	
250 255 260	
gat cta cgc gat gat atc gca gag atg gct gcg gaa ttc cgc gaa cgc	931
Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg	
265 270 275	
aat ctg acc tca gac atc att gag cgc aat gac gtc tac gct gca aag	979
Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys	
280 285 290	
ctt caa gtg ctg cgc gcc att ttt gaa atg cct cgt tcc agc gaa cgt	1027
Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg	
295 300 305	
gaa gcc aac ttt gtc tcc ttc gtg caa cgg gaa ggc caa ggt ctt att	1075
Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile	
310 315 320 325	
gat ttc gcc acc tgg tgc gcg gac cgc gaa act gca cag tct gaa tct	1123
Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser	
330 335 340	
gtc cac gga act gag cca gac cgc gat gag ctg acc atg ttc tac atg	1171
Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met	
345 350 355	
tgg ttg cag tgg cta tgt gat gag cag ctg gcg gca gct caa aag cgc	1219
Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Gln Lys Arg	
360 365 370	
gct gtc gat gcc gga atg tcg atc ggc atc atg gca gac ctg gca gtt	1267
Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val	
375 380 385	
ggt gtg cat cca ggt ggt gct gat gcc cag aac ctc agc cac gta ctt	1315
Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu	
390 395 400 405	
gct ccg gat gcg tca gtg ggc gcc cca cca gat gga tac aac cag cag	1363
Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln	
410 415 420	
ggc caa gac tgg tcc cag cca cca tgg cat cca gtg cgt ctt gca gag	1411
Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu	
425 430 435	
gaa ggc tac att ccg tgg cgt aat ctg ctg cgc act gtg ctg cgt cac	1459
Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His	
. 440 445 450	
tcc ggc gga atc cgc gtg gac cac gtt ctt ggt ttg ttc agg ctc ttt	1507
Ser Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe	
455 460 465	
gtc atg cca cgc atg caa tcc cct gct acg ggc acc tat atc cgc ttc	1555



Val 470	Met	Pro	Arg	Met 475	Gln	Ser	Pro	Ala	Thr	Gly 480	Thr	Tyr	Ile	Arg	Phe 485	
gac	cat	aat	gcg	ttg	gta	ggc	att	cta	gcc	cta	gaa	gca	gaa	ctc	gca	1603
Asp	His	Asn	Ala	Leu 490	Val	Gly	Ile	Leu	Ala	Leu	Glu	Ala	Glu	Leu	Ala	500
ggc	gcc	gtt	gtc	att	ggt	gaa	gat	ctg	gga	acg	ttt	gag	cct	tgg	gta	1651
Gly	Ala	Val	Val	Ile 505	Gly	Glu	Asp	Leu	Gly	Thr	Phe	Glu	Pro	Trp	Val	515
caa	gat	gca	ttg	gct	cag	cgt	ggc	atc	atg	ggc	acc	tcg	atc	cta	tgg	1699
Gln	Asp	Ala	Leu	Ala	Gln	Arg	Gly 525	Ile	Met	Gly	Thr	Ser	Ile	Leu	Trp	530
ttc	gag	cat	tcc	cca	agc	cag	ccg	ggt	cct	cgc	cgc	cag	gaa	gag	tat	1747
Phe	Glu	His	Ser	Pro	Ser	Gln	Pro	Gly	Pro	Arg	Arg	Gln	Glu	Glu	Tyr	545
cgt	ccg	ctg	gcc	ttg	acc	act	gtg	acc	act	cat	gat	ctc	cct	ccg	act	1795
Arg	Pro	Leu	Ala	Leu	Thr	Thr	Val	Thr	Thr	His	Asp	Leu	Pro	Pro	Thr	565
gct	ggt	tat	ttg	gag	ggc	gag	cac	att	gct	ctt	cgt	gag	cga	ttg	ggg	1843
Ala	Gly	Tyr	Leu	Glu 570	Gly	Glu	His	Ile	Ala	Leu	Arg	Glu	Arg	Leu	Gly	580
gtg	ctc	aac	act	gat	cct	gct	gca	gaa	ctc	gct	gag	gat	ctg	cag	tgg	1891
Val	Leu	Asn	Thr	Asp	Pro	Ala	Ala	Glu	Leu	Ala	Glu	Asp	Leu	Gln	Trp	595
caa	gcg	gag	atc	ctt	gat	gtc	gca	gca	tct	gcc	aac	gca	ttg	cca	gcc	1939
Gln	Ala	Glu	Ile	Leu	Asp	Val	Ala	Ala	Ser	Ala	Asn	Ala	Leu	Pro	Ala	610
cgg	gaa	tac	gtg	gga	ctc	gaa	cgc	gat	cag	cgc	ggt	gag	ttg	gct	gag	1987
Arg	Glu	Tyr	Val	Gly	Leu	Glu	Arg	Asp	Gln	Arg	Gly	Glu	Leu	Ala	Glu	625
ctg	ttg	gaa	ggc	ctg	cac	act	ttc	gtt	gcg	aaa	acc	cct	tca	gca	ctg	2035
Leu	Leu	Glu	Gly	Leu	His	Thr	Phe	Val	Ala	Lys	Thr	Pro	Ser	Ala	Leu	645
acc	tgt	gtc	tgc	ttg	gta	gac	atg	gtc	ggt	gaa	aag	cgg	gca	cag	aat	2083
Thr	Cys	Val	Cys	Leu 650	Val	Asp	Met	Val	Gly	Glu	Lys	Arg	Ala	Gln	Asn	660
cag	ccg	ggc	aca	acg	agg	gat	atg	tat	ccc	aac	tgg	tgt	atc	cca	ctg	2131
Gln	Pro	Gly	Thr	Thr	Arg	Asp	Met	Tyr	Pro	Asn	Trp	Cys	Ile	Pro	Leu	675
tgt	gac	agc	gaa	ggc	aac	tcc	gtg	ctc	att	gaa	tcg	ctg	cgt	gaa	aat	2179
Cys	Asp	Ser	Glu	Gly	Asn	Ser	Val	Leu	Ile	Glu	Ser	Leu	Arg	Glu	Asn	690
gag	ctg	tat	cac	cgt	gtg	gca	aag	gca	agc	aag	cga	gat	taggtccgct			2228
Glu	Leu	Tyr	His	Arg	Val	Ala	Lys	Ala	Ser	Lys	Arg	Asp				705
tcagttgtgg	tg															2241

<210> 410  
 <211> 706  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 410  
 Val Thr Ala Arg Arg Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val  
 1 5 10 15  
 Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp  
 20 25 30  
 Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr  
 35 40 45  
 Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe  
 50 55 60  
 His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val  
 65 70 75 80  
 Glu Gly Asp Glu Leu Val Phe Pro Val His Val His Asp Gly Ser Pro  
 85 90 95  
 Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser  
 100 105 110  
 Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp  
 115 120 125  
 Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His  
 130 135 140  
 Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile  
 145 150 155 160  
 Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro  
 165 170 175  
 Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser  
 180 185 190  
 Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val  
 195 200 205  
 Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala  
 210 215 220  
 Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg  
 225 230 235 240  
 Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe  
 245 250 255  
 Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala  
 260 265 270  
 Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp  
 275 280 285

Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro  
 290 295 300  
 Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu  
 305 310 315 320  
 Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr  
 325 330 335  
 Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu  
 340 345 350  
 Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala  
 355 360 365  
 Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met  
 370 375 380  
 Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn  
 385 390 395 400  
 Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp  
 405 410 415  
 Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro  
 420 425 430  
 Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg  
 435 440 445  
 Thr Val Leu Arg His Ser Gly Gly Ile Arg Val Asp His Val Leu Gly  
 450 455 460  
 Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln Ser Pro Ala Thr Gly  
 465 470 475 480  
 Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val Gly Ile Leu Ala Leu  
 485 490 495  
 Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr  
 500 505 510  
 Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly  
 515 520 525  
 Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg  
 530 535 540  
 Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr Thr Val Thr Thr His  
 545 550 555 560  
 Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu  
 565 570 575  
 Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala  
 580 585 590  
 Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala  
 595 600 605  
 Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg

610				615				620							
Gly 625	Glu	Leu	Ala	Glu	Leu	Leu	Glu	Gly	Leu	His 635	Thr	Phe	Val	Ala	Lys 640
Thr	Pro	Ser	Ala	Leu 645	Thr	Cys	Val	Cys	Leu 650	Val	Asp	Met	Val	Gly 655	Glu
Lys	Arg	Ala	Gln 660	Asn	Gln	Pro	Gly	Thr 665	Thr	Arg	Asp	Met	Tyr 670	Pro	Asn
Trp	Cys	Ile 675	Pro	Leu	Cys	Asp	Ser 680	Glu	Gly	Asn	Ser	Val 685	Leu	Ile	Glu
Ser 690	Leu	Arg	Glu	Asn	Glu	Leu 695	Tyr	His	Arg	Val	Ala 700	Lys	Ala	Ser	Lys
Arg 705	Asp														

```
<210> 411
<211> 2223
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(2200)
<223> FRXA00879
```

<400> 411																		
aaaagatgta ttttctaaca aacttacctt cagcgtacaa atatgctgtg cccacacgct																		60
attagtggca taatgttgtg ttgtgactgc tcgcagattt ttg aat gaa ctc gcc																		115
														Leu Asn Glu Leu Ala	5			
																		1
gat ctc tac ggc gta gca act tcc tac act gat tac aaa ggt gcc cat																		163
Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His																		
														10	15	20		
att gag gtc agc gat gac aca tta gtg aaa atc ctg cgt gct ctg ggt																		211
Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly																		
														25	30	35		
gtg aat tta gat aca agc aac ctc ccc aac gat gac gct atc caa cgc																		259
Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg																		
														40	45	50		
caa att gcc ctc ttc cat gat cga gag ttc act cgc cca ctg cct cca																		307
Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro																		
														55	60	65		
tcg gtg gtt gca gtt gaa ggt gat gaa cta gtt ttc ccg gtg cat gtg																		355
Ser Val Val Ala Val Glu Gly Asp Glu Leu Val Phe Pro Val His Val																		
														70	75	80	85	
cac gac ggt tcc cct gca gat gtc cac atc gaa ttg gaa gac ggc acg																		403
His Asp Gly Ser Pro Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr																		
														90	95	100		

cag cgg gat gtt tct cag gtg gaa aac tgg aca gcg cca cgg gaa att	451
Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile	
105 110 115	
gat ggg att agg tgg ggc gag gca tgc ttt aag att cct ggt gat ctc	499
Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu	
120 125 130	
ccc ttg ggt tgg cac aag ctt cac ctt aaa tcc aat gaa cgc tca gct	547
Pro Leu Gly Trp His Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala	
135 140 145	
gag tgc ggt ttg atc atc acc ccg gct cgt ctg tct act gct gat aag	595
Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys	
150 155 160 165	
tat ctt gat tcc cct cgc agt ggt gtc atg gcg cag atc tac tct gtg	643
Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val	
170 175 180	
cgt tcc acg ttg tgc tgg ggc atg ggt gat ttc aat gat tta gga aac	691
Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn	
185 190 195	
ttg gca agt gtg gtt gcc cag gat gga gca gac ttc ctg ctc atc aac	739
Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn	
200 205 210	
ccc atg cac gct gca gag ccg ctg cct cct act gag gac tct cct tat	787
Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr	
215 220 225	
ctg ccc aca acc agg cgc ttt atc aac ccg atc tac att cgg gta gaa	835
Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu	
230 235 240 245	
gat att ccg gag ttt aat cag ctt gag att gat cta cgc gat gat atc	883
Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile	
250 255 260	
gca gag atg gct gcg gaa ttc cgc gaa cgc aat ctg acc tca gac atc	931
Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile	
265 270 275	
att gag cgc aat gac gtc tac gct gca aag ctt caa gtg ctg cgc gcc	979
Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala	
280 285 290	
att ttt gaa atg cct cgt tcc agc gaa cgt gaa gcc aac ttt gtc tcc	1027
Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser	
295 300 305	
ttc gtg caa cgg gaa ggc caa ggt ctt att gat ttc gcc acc tgg tgc	1075
Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys	
310 315 320 325	
gcg gac cgc gaa act gca cag tct gaa tct gtc cac gga act gag cca	1123
Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro	
330 335 340	

gac cgc gat gag ctg acc atg ttc tac atg tgg ttg cag tgg cta tgt	1171
Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys	
345 350 355	
gat gag cag ctg gcg gca gct caa aag cgc gct gtc gat gcc gga atg	1219
Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met	
360 365 370	
tcg atc ggc atc atg gca gac ctg gca gtt ggt gtg cat cca ggt ggt	1267
Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly Val His Pro Gly Gly	
375 380 385	
gct gat gcc cag aac ctc agc cac gta ctt gct ccg gat gcg tca gtg	1315
Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala Pro Asp Ala Ser Val	
390 395 400 405	
ggc gcc cca cca gat gga tac aac cag cag ggc caa gac tgg tcc cag	1363
Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln	
410 415 420	
cca cca tgg cat cca gtg cgt ctt gca gag gaa ggc tac att ccg tgg	1411
Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp	
425 430 435	
cgt aat ctg ctg cgc act gtg ctg cgt cac tcc ggc gga atc cgc gtg	1459
Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser Gly Gly Ile Arg Val	
440 445 450	
gac cac gtt ctt ggt ttg ttc agg ctc ttt gtc atg cca cgc atg caa	1507
Asp His Val Leu Gly Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln	
455 460 465	
tcc cct gct acg ggc acc tat atc cgc ttc gac cat aat gcg ttg gta	1555
Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val	
470 475 480 485	
ggc att cta gcc cta gaa gca gaa ctc gca ggc gcc gtt gtc att ggt	1603
Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly	
490 495 500	
gaa gat ctg gga acg ttt gag cct tgg gta caa gat gca ttg gct cag	1651
Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln	
505 510 515	
cgt ggc atc atg ggc acc tcg atc cta tgg ttc gag cat tcc cca agc	1699
Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser	
520 525 530	
cag ccg ggt cct cgc cgc cag gaa gag tat cgt ccg ctg gcc ttg acc	1747
Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr	
535 540 545	
act gtg acc act cat gat ctc cct ccg act gct ggt tat ttg gag ggc	1795
Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly	
550 555 560 565	
gag cac att gct ctt cgt gag cga ttg ggg gtg ctc aac act gat cct	1843
Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro	
570 575 580	
gct gca gaa ctc gct gag gat ctg cag tgg caa gcg gag atc ctt gat	1891

Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp  
585 590 595

gtc gca gca tct gcc aac gca ttg cca gcc cgg gaa tac gtg gga ctc 1939  
Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu  
600 605 610

gaa cgc gat cag cgc ggt gag ttg gct gag ctg ttg gaa ggc ctg cac 1987  
Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His  
615 620 625

act ttc gtt gcg aaa acc cct tca gca ctg acc tgt gtc tgc ttg gta 2035  
Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val  
630 635 640 645

gac atg gtc ggt gaa aag cgg gca cag aat cag ccg ggc aca acg agg 2083  
Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg  
650 655 660

gat atg tat ccc aac tgg tgt atc cca ctg tgt gac agc gaa ggc aac 2131  
Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn  
665 670 675

tcc gtg ctc att gaa tcg ctg cgt gaa aat gag ctg tat cac cgt gtg 2179  
Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val  
680 685 690

gca aag gca agc aag cga gat taggtccgct tcagttgtgg tgg 2223  
Ala Lys Ala Ser Lys Arg Asp  
695 700

&lt;210&gt; 412

&lt;211&gt; 700

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 412

Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp  
1 5 10 15

Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile  
20 25 30

Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp  
35 40 45

Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr  
50 55 60

Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu Val  
65 70 75 80

Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile Glu  
85 90 95

Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr  
100 105 110

Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys  
115 120 125

Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys Ser  
 130 135 140  
 Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu  
 145 150 155 160  
 Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala  
 165 170 175  
 Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe  
 180 185 190  
 Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp  
 195 200 205  
 Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr  
 210 215 220  
 Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile  
 225 230 235 240  
 Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp  
 245 250 255  
 Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn  
 260 265 270  
 Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu  
 275 280 285  
 Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu  
 290 295 300  
 Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp  
 305 310 315 320  
 Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val  
 325 330 335  
 His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp  
 340 345 350  
 Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala  
 355 360 365  
 Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly  
 370 375 380  
 Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala  
 385 390 395 400  
 Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly  
 405 410 415  
 Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu  
 420 425 430  
 Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser  
 435 440 445



Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val  
 450 455 460  
 Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp  
 465 470 475 480  
 His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly  
 485 490 495  
 Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln  
 500 505 510  
 Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe  
 515 520 525  
 Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg  
 530 535 540  
 Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala  
 545 550 555 560  
 Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val  
 565 570 575  
 Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln  
 580 585 590  
 Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg  
 595 600 605  
 Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu  
 610 615 620  
 Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr  
 625 630 635 640  
 Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln  
 645 650 655  
 Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys  
 660 665 670  
 Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu  
 675 680 685  
 Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp  
 690 695 700

&lt;210&gt; 413

&lt;211&gt; 1287

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1264)

&lt;223&gt; RXN00043

&lt;400&gt; 413

aacagcaggc ctcaagtccg aagataatta acctaaatcc gtagacataa gacatcatac 60

gtcctatgct tgctggaagg aagcaaataa cctcagaaaag atg gca gaa gtg gtg 115  
Met Ala Glu Val Val  
1 5

cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga 163  
His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg  
10 15 20

att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac 211  
Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn  
25 30 35

ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga 259  
Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly  
40 45 50

ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat 307  
Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His  
55 60 65

aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag 355  
Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln  
70 75 80 85

gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg 403  
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met  
90 95 100

ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg 451  
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val  
105 110 115

gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac 499  
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His  
120 125 130

ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg 547  
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro  
135 140 145

gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat 595  
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His  
150 155 160 165

gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac 643  
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp  
170 175 180

aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct 691  
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala  
185 190 195

tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att 739  
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile  
200 205 210

gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc 787  
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe  
215 220 225

aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct	835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala	
230 235 240 245	
ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc	883
Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala	
250 255 260	
gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac	931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn	
265 270 275	
aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac	979
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp	
280 285 290	
ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc	1027
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val	
295 300 305	
gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta	1075
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu	
310 315 320 325	
gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac	1123
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp	
330 335 340	
gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc	1171
Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser	
345 350 355	
gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac	1219
Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp	
360 365 370	
tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att	1264
Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile	
375 380 385	
taaatacgag caaaactttc ctg	1287

&lt;210&gt; 414

&lt;211&gt; 388

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 414

Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys
1 5 10 15

Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe
20 25 30

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
35 40 45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr  
 65 70 75 80  
 Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His  
 85 90 95  
 Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala  
 100 105 110  
 Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu  
 115 120 125  
 Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys  
 130 135 140  
 Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu  
 145 150 155 160  
 Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val  
 165 170 175  
 Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala  
 180 185 190  
 His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr  
 195 200 205  
 Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr  
 210 215 220  
 Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro  
 225 230 235 240  
 Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr  
 245 250 255  
 Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp  
 260 265 270  
 Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala  
 275 280 285  
 Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr  
 290 295 300  
 Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly  
 305 310 315 320  
 Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly  
 325 330 335  
 Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys  
 340 345 350  
 Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn  
 355 360 365  
 Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp  
 370 375 380  
 His Gln Val Ile



Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile	
200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	
aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct	835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala	
230 235 240 245	
ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc	883
Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala	
250 255 260	
gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac	931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn	
265 270 275	
aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac	979
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp	
280 285 290	
ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc	1027
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val	
295 300 305	
gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta	1075
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu	
310 315 320 325	
gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac	1123
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp	
330 335 340	
gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc	1171
Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser	
345 350 355	
gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac	1219
Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp	
360 365 370	
tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att	1264
Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile	
375 380 385	
taaatacgag caaaactttc ctg	1287
<210> 416	
<211> 388	
<212> PRT	

<213> *Corynebacterium glutamicum*

&lt;400&gt; 416

Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys  
 1 5 10 15  
 Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe  
 20 25 30  
 Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala  
 35 40 45  
 Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser  
 50 55 60  
 Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr  
 65 70 75 80  
 Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His  
 85 90 95  
 Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala  
 100 105 110  
 Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu  
 115 120 125  
 Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys  
 130 135 140  
 Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu  
 145 150 155 160  
 Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val  
 165 170 175  
 Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala  
 180 185 190  
 His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr  
 195 200 205  
 Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr  
 210 215 220  
 Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro  
 225 230 235 240  
 Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr  
 245 250 255  
 Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp  
 260 265 270  
 Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala  
 275 280 285  
 Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr  
 290 295 300  
 Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly

```
<210> 417
<211> 1584
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1561)  
<223> RXN01752
```

602



105							110					115					
aag	ctg	aaa	acc	tac	acg	gtg	tgt	gtg	ccc	gcc	tat	ggc	gaa	cct	gag	499	
Lys	Leu	Lys	Thr	Tyr	Thr	Val	Leu	Val	Pro	Ala	Tyr	Gly	Glu	Pro	Glu		
		120					125					130					
gtg	att	gcg	cag	ctg	ctg	gca	tcc	atg	cac	gct	ttt	gat	tac	ccc	aag	547	
Val	Ile	Ala	Gln	Leu	Leu	Ala	Ser	Met	His	Ala	Phe	Asp	Tyr	Pro	Lys		
	135					140					145						
cat	ctt	ctg	cag	gta	ttg	ctc	atg	ttg	gag	gaa	gat	gat	ctg	ccc	acg	595	
His	Leu	Leu	Gln	Val	Leu	Leu	Met	Leu	Glu	Glu	Asp	Asp	Leu	Pro	Thr		
150					155					160					165		
atc	gcc	gcg	gca	gag	gca	gcg	gga	gtg	gat	cag	gtg	gca	acg	atc	att	643	
Ile	Ala	Ala	Ala	Glu	Ala	Ala	Gly	Val	Asp	Gln	Val	Ala	Thr	Ile	Ile		
				170					175					180			
aag	gtg	ccg	cca	gcg	cag	ccc	cgc	acc	aag	ccg	aag	gcc	tgt	aac	tat	691	
Lys	Val	Pro	Pro	Ala	Gln	Pro	Arg	Thr	Lys	Pro	Lys	Ala	Cys	Asn	Tyr		
			185					190					195				
gga	ttg	cac	ttt	gcc	acg	ggg	gaa	att	gtc	acg	atc	ttt	gac	gcg	gaa	739	
Gly	Leu	His	Phe	Ala	Thr	Gly	Glu	Ile	Val	Thr	Ile	Phe	Asp	Ala	Glu		
		200					205					210					
gac	atg	cca	gat	ccc	ctc	caa	ctg	cgt	cgc	gtg	gtg	gtg	gca	ttt	gaa	787	
Asp	Met	Pro	Asp	Pro	Leu	Gln	Leu	Arg	Arg	Val	Val	Val	Ala	Phe	Glu		
	215					220					225						
cgc	tcg	gct	tcc	aat	acg	gtg	tgc	gtc	cag	tca	agg	ttg	tcg	tat	cga	835	
Arg	Ser	Ala	Ser	Asn	Thr	Val	Cys	Val	Gln	Ser	Arg	Leu	Ser	Tyr	Arg		
230					235					240					245		
aac	gcc	agg	cag	aat	ctg	cta	act	gcg	tgg	ttc	acc	att	gaa	tat	gac	883	
Asn	Ala	Arg	Gln	Asn	Leu	Leu	Thr	Ala	Trp	Phe	Thr	Ile	Glu	Tyr	Asp		
				250					255					260			
gtg	tgg	ttt	aac	ttc	ctg	ctg	cca	ggc	gtc	atg	cgc	atg	aac	gca	cct	931	
Val	Trp	Phe	Asn	Phe	Leu	Leu	Pro	Gly	Val	Met	Arg	Met	Asn	Ala	Pro		
			265					270					275				
gtc	cca	ttg	ggc	ggt	acc	tcc	aac	cat	ctg	ctc	acg	ggt	gtc	ctg	aaa	979	
Val	Pro	Leu	Gly	Gly	Thr	Ser	Asn	His	Leu	Leu	Thr	Gly	Val	Leu	Lys		
		280					285					290					
gat	ctc	ggc	gcg	tgg	gat	cct	ttc	aat	gtc	aca	gaa	aat	gcc	gac	ctc	1027	
Asp	Leu	Gly	Ala	Trp	Asp	Pro	Phe	Asn	Val	Thr	Glu	Asn	Ala	Asp	Leu		
		295				300					305						
ggc	gta	ccc	atc	gcg	gca	aaa	gga	tat	tcc	acc	gcg	gtg	ttg	gat	tcg	1075	
Gly	Val	Pro	Ile	Ala	Ala	Lys	Gly	Tyr	Ser	Thr	Ala	Val	Leu	Asp	Ser		
310					31												

cgc agg cca aag tgg tta gtc caa gag ctt ggc atc att cct gct gtg 1219  
 Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val  
 360 365 370  
 cgt ttt acc ttc ctc atg gca ggc acc ccg atc att gcg gtg ctc aat 1267  
 Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn  
 375 380 385  
 ctg ctc ttt tgg tac ttg tcg ctc acg tgg att ctg ggc cag ccc ggc 1315  
 Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly  
 390 395 400 405  
 acc att gag cag atg ttc cca cct gcg gtg tac tac cca gcg ttg gtg 1363  
 Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val  
 410 415 420  
 tgt ttg gtg gtg gcc aat gct gcg acc atc ttt atg aat ctc att ggc 1411  
 Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly  
 425 430 435  
 tgc cgg gaa ggc cgc gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc 1459  
 Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe  
 440 445 450  
 ccg ctg tat tgg ctg ctc atg agc att gca gcg ttg aaa ggc acg tgg 1507  
 Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp  
 455 460 465  
 caa ttg atc acg cga cca tcc tat tgg gag aaa act gcc cac gga ttg 1555  
 Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu  
 470 475 480 485  
 gag gcg taagcgggtgc ccacgtcaa acc 1584  
 Glu Ala

&lt;210&gt; 418

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 418

Met Met Glu Gln Asp Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala  
 1 5 10 15  
 Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu  
 20 25 30  
 Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly  
 35 40 45  
 Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu  
 50 55 60  
 Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr  
 65 70 75 80  
 Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg  
 85 90 95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu  
 100 105 110  
 Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala  
 115 120 125  
 Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala  
 130 135 140  
 Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu  
 145 150 155 160  
 Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln  
 165 170 175  
 Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro  
 180 185 190  
 Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr  
 195 200 205  
 Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val  
 210 215 220  
 Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser  
 225 230 235 240  
 Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe  
 245 250 255  
 Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met  
 260 265 270  
 Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu  
 275 280 285  
 Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr  
 290 295 300  
 Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr  
 305 310 315 320  
 Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile  
 325 330 335  
 Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr  
 340 345 350  
 Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly  
 355 360 365  
 Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile  
 370 375 380  
 Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile  
 385 390 395 400  
 Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr  
 405 410 415

Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe  
 420 425 430

Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile  
 435 440 445

Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala  
 450 455 460

Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys  
 465 470 475 480

Thr Ala His Gly Leu Glu Ala  
 485

<210> 419  
 <211> 689  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (19)..(666)  
 <223> FRXA01839

<400> 419  
 ttcctgtctgc caggtgtcatg cgc atg aac gca cct gtc cca ttg ggc ggt 51  
 Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly  
 1 5 10

acc tcc aac cat ctg ctc acg ggt gtc ctg aaa gat ctc ggc gcg tgg 99  
 Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp  
 15 20 25

gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg 147  
 Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala  
 30 35 40

gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa 195  
 Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu  
 45 50 55

gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243  
 Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr  
 60 65 70 75

aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg 291  
 Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp  
 80 85 90

tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339  
 Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu  
 95 100 105

atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac 387  
 Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Phe Trp Tyr  
 110 115 120

ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg 435  
 Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met

125	130	135	
ttc cca cct gcg gtg tac tac cca gcg ttg gtg tgt ttg gtg gtg gcc			483
Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala			
140	145	150	155
aat gct gcg acc atc ttt atg aat ctc att ggc tgc cgg gaa ggc cgc			531
Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg			
	160	165	170
gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc ccg ctg tat tgg ctg			579
Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu			
	175	180	185
ctc atg agc att gca gcg ttg aaa ggc acg tgg caa ttg atc acg cga			627
Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg			
	190	195	200
cca tcc tat tgg gag aaa act gcc cac gga ttg gag gcg taagcgggtgc			676
Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu Glu Ala			
205	210	215	
ccatcgtcaa acc			689
<210> 420			
<211> 216			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 420			
Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu			
1	5	10	15
Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val			
	20	25	30
Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala Ala Lys Gly Tyr Ser			
	35	40	45
Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr			
	50	55	60
Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln			
65	70	75	80
Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu			
	85	90	95
Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro			
	100	105	110
Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp			
	115	120	125
Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val			
	130	135	140
Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile			
145	150	155	160

<400> 421															
tacgcccagg gtttccatat tggtaaattct aagccgattg atgaatttat agctacttat															60
ctcgagacga accaaaccgc tacctggggg taggaagaat atg aaa aag aag agc															115
Met Lys Lys Lys Ser															
1 5															
ttt cca atc gca aga gtc atc ggt atc ggc gtc ctt ggc atc gcc ggg															163
Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val Leu Gly Ile Ala Gly															
10 15 20															
atg gga ata ttg ttg cta tgg ctt gca gtt acc ctg tct gat cca gca															211
Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr Leu Ser Asp Pro Ala															
25 30 35															
tca ccg ggt gcc aaa gaa acc gaa gtc ttt gat agg tgg aaa gtg ctc															259
Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp Arg Trp Lys Val Leu															
40 45 50															
ttt gat gac tat att cca cca gtc agg gta ttg gtt gct gcg att atc															307
Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu Val Ala Ala Ile Ile															
55 60 65															
gtt gca tta att ttc gtc ttt atc gct gcc aca gtg gaa cga acc gta															355
Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr Val Glu Arg Thr Val															
70 75 80 85															
acc aac cgc tac cga agc tcc gta gac ggc gaa aga gtg cca tta gcg															403
Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu Arg Val Pro Leu Ala															
90 95 100															
ccg aag att gtg atg gca gaa acc cga ggg gta ttt cat gga ccg att															451
Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val Phe His Gly Pro Ile															
105 110 115															
acc att aac gtg ctc gtg cca gca cac aat gag gcg gaa aga att act															499
Thr Ile Asn Val Leu Val Pro Ala His Asn Glu Ala Glu Arg Ile Thr															
120 125 130															

gga aca att cag gca ttg aaa tca caa cat gag cct cca gaa cgc atc 547  
 Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu Pro Pro Glu Arg Ile  
 135 140 145

gtt gta gtt gcc gat aat tgc act gat gaa act acg gaa tta gcc cgt 595  
 Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr Thr Glu Leu Ala Arg  
 150 155 160 165

gct gag gga gtg gag gtc ttg gaa aca gtc aat aat aag ttt aag aag 643  
 Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn Asn Lys Phe Lys Lys  
 170 175 180

gcc gga gga ctc aat cag gct ttg agc cgg atg ctt ccc aca ttg ggg 691  
 Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met Leu Pro Thr Leu Gly  
 185 190 195

gag aat gac att gtg atg atc gtt gac gct gat aca gca ctt gat caa 739  
 Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp Thr Ala Leu Asp Gln  
 200 205 210

ggt ttc ctc aag gaa gca cgg cgc cgc ttt gag tct gat cgc gct cta 787  
 Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu Ser Asp Arg Ala Leu  
 215 220 225

atg gcc gtg ggc gga ttg ttc tac ggt gag tca ggc tcc gga tgg ctt 835  
 Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser Gly Ser Gly Trp Leu  
 230 235 240 245

ggc caa tat cag cgc aac gaa tac acc cgt tat agc cgt gac atc tat 883  
 Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr Ser Arg Asp Ile Tyr  
 250 255 260

cga cgc cgc gga cgt gtg ttt gtt ttg act gga aca gcg tcg gct ttt 931  
 Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly Thr Ala Ser Ala Phe  
 265 270 275

cgg cca cgc ggc ctg cgg aca gta gcg gaa tca cgc ggg aca ttg atc 979  
 Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser Arg Gly Thr Leu Ile  
 280 285 290

ccc gga cgt aaa gcc gat gtt tat gac acc gcg ggc gtt gac cga aga 1027  
 Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala Gly Val Asp Arg Arg  
 295 300 305

taatgagttg accctggctt tga 1050

&lt;210&gt; 422

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 422

Met Lys Lys Lys Ser Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val  
 1 5 10 15

Leu Gly Ile Ala Gly Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr  
 20 25 30

Leu Ser Asp Pro Ala Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp

35                      40                      45  
 Arg Trp Lys Val Leu Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu  
     50                      55                      60  
 Val Ala Ala Ile Ile Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr  
     65                      70                      75                      80  
 Val Glu Arg Thr Val Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu  
                     85                      90                      95  
 Arg Val Pro Leu Ala Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val  
                     100                      105                      110  
 Phe His Gly Pro Ile Thr Ile Asn Val Leu Val Pro Ala His Asn Glu  
                     115                      120                      125  
 Ala Glu Arg Ile Thr Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu  
                     130                      135                      140  
 Pro Pro Glu Arg Ile Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr  
     145                      150                      155                      160  
 Thr Glu Leu Ala Arg Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn  
                     165                      170                      175  
 Asn Lys Phe Lys Lys Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met  
                     180                      185                      190  
 Leu Pro Thr Leu Gly Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp  
                     195                      200                      205  
 Thr Ala Leu Asp Gln Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu  
                     210                      215                      220  
 Ser Asp Arg Ala Leu Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser  
     225                      230                      235                      240  
 Gly Ser Gly Trp Leu Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr  
                     245                      250                      255  
 Ser Arg Asp Ile Tyr Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly  
                     260                      265                      270  
 Thr Ala Ser Ala Phe Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser  
                     275                      280                      285  
 Arg Gly Thr Leu Ile Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala  
                     290                      295                      300  
 Gly Val Asp Arg Arg  
     305

&lt;210&gt; 423

&lt;211&gt; 882

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS



&lt;222&gt; (101)..(859)

&lt;223&gt; RXA00042

&lt;400&gt; 423

gtggtctttg actcaaacgg ccagttacaa cagggtccatt tagaccatca agtaatttaa 60

atac	gag	caa	aactttc	ctg	ataataaaa	gag	gtccg	acc	atg	gac	atc	atc	atc	115
									Met	Asp	Ile	Ile	Ile	
									1				5	

tgc	aaa	gac	gag	caa	gaa	gtc	ggc	aaa	gca	gcg	gca	gcc	ctg	atc	gca	163
Cys	Lys	Asp	Glu	Gln	Glu	Val	Gly	Lys	Ala	Ala	Ala	Ala	Leu	Ile	Ala	
				10					15				20			

ccc	ttc	gca	act	aag	ggc	gga	acc	ttg	ggg	ctt	gca	act	gga	tcg	tca	211
Pro	Phe	Ala	Thr	Lys	Gly	Gly	Thr	Leu	Gly	Leu	Ala	Thr	Gly	Ser	Ser	
			25					30					35			

cct	ttg	agc	acc	tac	caa	gag	ctc	att	cgc	atg	tat	gaa	gct	ggg	gaa	259
Pro	Leu	Ser	Thr	Tyr	Gln	Glu	Leu	Ile	Arg	Met	Tyr	Glu	Ala	Gly	Glu	
			40				45					50				

gtg	tca	ttc	aag	aac	tgc	aag	gca	ttc	ttg	ttg	gat	gaa	tac	gtg	gga	307
Val	Ser	Phe	Lys	Asn	Cys	Lys	Ala	Phe	Leu	Leu	Asp	Glu	Tyr	Val	Gly	
		55				60					65					

tta	acg	cgc	gac	gat	gaa	aac	agc	tac	ttc	aaa	acc	att	cgt	aaa	gag	355
Leu	Thr	Arg	Asp	Asp	Glu	Asn	Ser	Tyr	Phe	Lys	Thr	Ile	Arg	Lys	Glu	
		70			75					80					85	

ttc	act	gac	cac	atc	gac	atc	gtt	gat	gaa	gag	gtc	tac	agc	cca	gat	403
Phe	Thr	Asp	His	Ile	Asp	Ile	Val	Asp	Glu	Glu	Val	Tyr	Ser	Pro	Asp	
			90					95						100		

ggc	gca	aac	cct	gat	cca	tac	gaa	gca	gct	gca	gag	tat	gag	gca	aag	451
Gly	Ala	Asn	Pro	Asp	Pro	Tyr	Glu	Ala	Ala	Ala	Glu	Tyr	Glu	Ala	Lys	
			105					110					115			

atc	gct	gca	gaa	tcc	gtt	gat	gtt	caa	atc	ctt	ggc	atc	ggc	gga	aac	499
Ile	Ala	Ala	Glu	Ser	Val	Asp	Val	Gln	Ile	Leu	Gly	Ile	Gly	Gly	Asn	
			120				125					130				

ggc	cac	atc	gct	ttc	aat	gag	cca	tca	tct	tct	ctg	tca	gga	ctg	aca	547
Gly	His	Ile	Ala	Phe	Asn	Glu	Pro	Ser	Ser	Ser	Leu	Ser	Gly	Leu	Thr	
		135				140					145					

aag	gtc	cag	gcg	ctg	cac	cct	aaa	act	gtg	gag	gac	aac	gct	cga	ttc	595
Lys	Val	Gln	Ala	Leu	His	Pro	Lys	Thr	Val	Glu	Asp	Asn	Ala	Arg	Phe	
		150			155					160					165	

ttc	aac	acc	atc	gaa	gag	gtc	cca	acc	cac	gcc	ctc	acc	cag	ggc	ttg	643
Phe	Asn	Thr	Ile	Glu	Glu	Val	Pro	Thr	His	Ala	Leu	Thr	Gln	Gly	Leu	
			170					175					180			

ggc	act	ttg	tcc	cgc	gcg	caa	aac	atc	gtg	ttg	gtg	gca	act	ggc	gaa	691
Gly	Thr	Leu	Ser	Arg	Ala	Gln	Asn	Ile	Val	Leu	Val	Ala	Thr	Gly	Glu	
			185				190					195				

gga	aaa	gcc	gac	gcc	atc	cgc	gga	act	gtg	gaa	ggc	cca	ctg	acc	gcc	739
Gly	Lys	Ala	Asp	Ala	Ile	Arg	Gly	Thr	Val	Glu	Gly	Pro	Leu	Thr	Ala	
		200					205					210				

atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc 787  
 Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile  
 215 220 225

gtt gat gaa gca gca gca tcc aag ctg gaa aac gct gat cac tac cgt 835  
 Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg  
 230 235 240 245

ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg 882  
 Leu Met Glu Gln Leu Lys Leu Arg  
 250

<210> 424

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Asp Ile Ile Ile Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala  
 1 5 10 15

Ala Ala Leu Ile Ala Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu  
 20 25 30

Ala Thr Gly Ser Ser Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met  
 35 40 45

Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu  
 50 55 60

Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys  
 65 70 75 80

Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu  
 85 90 95

Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala  
 100 105 110

Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu  
 115 120 125

Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser  
 130 135 140

Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu  
 145 150 155 160

Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala  
 165 170 175

Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu  
 180 185 190

Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu  
 195 200 205

Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn  
 210 215 220

Asn Ala Thr Ile Ile Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn  
 225 230 235 240

Ala Asp His Tyr Arg Leu Met Glu Gln Leu Lys Leu Arg  
 245 250

<210> 425  
 <211> 1998  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1975)  
 <223> RXA01482

<400> 425  
 ttgcgtgctg caacttaatt atggctcctcc cagctcagtg tgctgtgtgg attgtttatt 60

ctcgtccatt aagtgatcga. gaaaaagttg ttgtaaagtc atg cgc atg tgt gga 115  
 Met Arg Met Cys Gly  
 1 5

att gtt gga tat att ggc caa gcg ggc gac tcc cgt gat tac ttt gct 163  
 Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser Arg Asp Tyr Phe Ala  
 10 15 20

cta gat gta gtt gtt gaa gga cta cgt cgc ctg gaa tac cgc gga tat 211  
 Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr  
 25 30 35

gac tcc gca ggt att gct att cac gcc aat ggt gag att agc tac cga 259  
 Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly Glu Ile Ser Tyr Arg  
 40 45 50

aag aag gcc gga aag gtt gct gca cta gat gca gaa atc gct aaa gca 307  
 Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala Glu Ile Ala Lys Ala  
 55 60 65

cct ctt cca gat tct att ttg gga att gga cac acc cgt tgg gca act 355  
 Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His Thr Arg Trp Ala Thr  
 70 75 80 85

cat ggt ggc cca acc gat gtc aac gct cac ccc cac gtt gtt tcc aat 403  
 His Gly Gly Pro Thr Asp Val Asn Ala His Pro His Val Val Ser Asn  
 90 95 100

ggc aag ctt gcc gta gta cac aac ggc atc atc gaa aac ttt gcg gaa 451  
 Gly Lys Leu Ala Val Val His Asn Gly Ile Ile Glu Asn Phe Ala Glu  
 105 110 115

ctg cgc tct gag ctt tcc gct aag ggc tac aac ttt gta tcc gat acc 499  
 Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn Phe Val Ser Asp Thr  
 120 125 130

gat acc gaa gtt gct gct tct ttg ctt gct gaa att tac aat act cag 547  
 Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu Ile Tyr Asn Thr Gln  
 135 140 145

gca aac ggt gac ctc acc ctt gct atg cag ctg acc ggt cag cgc ctt	595
Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu Thr Gly Gln Arg Leu	
150 155 160 165	
gag ggt gct ttc acc ctg cta gct att cat gct gat cac gat gac cgc	643
Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala Asp His Asp Asp Arg	
170 175 180	
atc gtt gca gct cgt cgt aac tct cct ttg gtt atc ggc gtc ggc gag	691
Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val Ile Gly Val Gly Glu	
185 190 195	
ggc gag aac ttc ctc gga tct gac gtt tct ggc ttt att gat tac acc	739
Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly Phe Ile Asp Tyr Thr	
200 205 210	
cgc aag gct gta gag ctg gct aat gac cag gtt gtt acc atc acc gct	787
Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val Val Thr Ile Thr Ala	
215 220 225	
gat gat tac gcc atc acc aac ttt gat gga tca gaa gca gtt ggc aag	835
Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser Glu Ala Val Gly Lys	
230 235 240 245	
cct ttc gac gtg gag tgg gac gct gca gct gct gaa aag ggt ggc ttc	883
Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala Glu Lys Gly Gly Phe	
250 255 260	
ggg tcc ttc atg gag aag gaa atc cac gat cag cca gca gct gtt cgc	931
Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln Pro Ala Ala Val Arg	
265 270 275	
gat acc ctg atg ggc cgt ctt gat gaa gat ggc aag ctc gtt ctt gat	979
Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly Lys Leu Val Leu Asp	
280 285 290	
gag ctg cgc atc gat gaa gct att ctg cgt agt gtc gac aag atc gtc	1027
Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser Val Asp Lys Ile Val	
295 300 305	
att gtt gct tgt ggt act gca gct tat gca ggc cag gtt gct cgt tac	1075
Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly Gln Val Ala Arg Tyr	
310 315 320 325	
gcc att gag cac tgg tgc cgc atc cca acc gag gtg gag ctg gct cac	1123
Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu Val Glu Leu Ala His	
330 335 340	
gag ttc cgt tac cgc gac cca atc ctc aac gag aag acc ctt gtt gtg	1171
Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu Lys Thr Leu Val Val	
345 350 355	
gca ttg tcc cag tcc ggc gag acc atg gat acc ctc atg gct gtt cgc	1219
Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr Leu Met Ala Val Arg	
360 365 370	
cac gca cgt gag cag ggt gcc aag gtt gtt gct att tgt aac act gtt	1267
His Ala Arg Glu Gln Gly Ala Lys Val Val Ala Ile Cys Asn Thr Val	
375 380 385	
gga tcc act ctt cca cgt gaa gca gat gcg tcc ctg tac acc tac gct	1315

Gly 390	Ser	Thr	Leu	Pro	Arg 395	Glu	Ala	Asp	Ala	Ser 400	Leu	Tyr	Thr	Tyr	Ala 405	
ggc	cct	gag	atc	gct	gtg	gcg	tcc	acc	aag	gcg	ttc	ttg	gct	cag	atc	1363
Gly	Pro	Glu	Ile	Ala	Val	Ala	Ser	Thr	Lys	Ala	Phe	Leu	Ala	Gln	Ile	
				410					415					420		
act	gct	tct	tac	ttg	ctt	ggc	ctg	tac	ttg	gct	cag	ctg	cgc	ggc	aac	1411
Thr	Ala	Ser	Tyr	Leu	Leu	Gly	Leu	Tyr	Leu	Ala	Gln	Leu	Arg	Gly	Asn	
			425					430					435			
aag	ttc	gct	gat	gag	gtt	tct	tcc	att	ctg	gac	agc	ctg	cgt	gag	atg	1459
Lys	Phe	Ala	Asp	Glu	Val	Ser	Ser	Ile	Leu	Asp	Ser	Leu	Arg	Glu	Met	
		440					445					450				
cct	gag	aag	att	cag	cag	gtc	atc	gat	gca	gaa	gag	cag	atc	aag	aag	1507
Pro	Glu	Lys	Ile	Gln	Gln	Val	Ile	Asp	Ala	Glu	Glu	Gln	Ile	Lys	Lys	
	455					460						465				
ctt	ggc	caa	gat	atg	gca	gat	gct	aag	tct	gtg	ctg	ttc	ctg	ggc	cgc	1555
Leu	Gly	Gln	Asp	Met	Ala	Asp	Ala	Lys	Ser	Val	Leu	Phe	Leu	Gly	Arg	
470					475					480					485	
cac	gtt	ggt	ttc	cca	gtt	gcg	ctt	gag	ggt	gcg	ttg	aag	ctc	aag	gag	1603
His	Val	Gly	Phe	Pro	Val	Ala	Leu	Glu	Gly	Ala	Leu	Lys	Leu	Lys	Glu	
				490					495					500		
atc	gca	tac	ctg	cac	gct	gaa	ggt	ttc	gct	gca	ggc	gag	ctc	aag	cac	1651
Ile	Ala	Tyr	Leu	His	Ala	Glu	Gly	Phe	Ala	Ala	Gly	Glu	Leu	Lys	His	
			505					510					515			
ggc	cca	att	gct	ttg	gtt	gag	gaa	ggc	cag	ccg	atc	ttc	gtt	atc	gtg	1699
Gly	Pro	Ile	Ala	Leu	Val	Glu	Glu	Gly	Gln	Pro	Ile	Phe	Val	Ile	Val	
		520				525						530				
cct	tca	cct	cgt	ggt	cgc	gat	tcc	ctg	cac	tcc	aag	gtt	gtc	tcc	aac	1747
Pro	Ser	Pro	Arg	Gly	Arg	Asp	Ser	Leu	His	Ser	Lys	Val	Val	Ser	Asn	
	535					540					545					
att	cag	gag	atc	cgt	gca	cgt	ggc	gct	gtc	acc	atc	gtg	att	gca	gag	1795
Ile	Gln	Glu	Ile	Arg	Ala	Arg	Gly	Ala	Val	Thr	Ile	Val	Ile	Ala	Glu	
550					555					560					565	
gaa	ggc	gat	gag	gct	gtc	aac	gat	tac	gcc	aac	ttc	atc	atc	cgc	att	1843
Glu	Gly	Asp	Glu	Ala	Val	Asn	Asp	Tyr	Ala	Asn	Phe	Ile	Ile	Arg	Ile	
				570					575					580		
cct	cag	gcc	cca	acc	ctg	atg	cag	cct	ctg	ctg	tcc	acc	gtg	cct	ctg	1891
Pro	Gln	Ala	Pro	Thr	Leu	Met	Gln	Pro	Leu	Leu	Ser	Thr	Val	Pro	Leu	
			585					590					595			
cag	atc	ttt	gcg	tgc	gct	gtg	gca	acc	gca	aag	ggc	tac	aac	gtg	gat	1939
Gln	Ile	Phe	Ala	Cys	Ala	Val	Ala	Thr	Ala	Lys	Gly	Tyr	Asn	Val	Asp	
		600					605					610				
cag	cct	cgt	aac	ctg	gca	aag	tct	gtc	acc	gtc	gaa	taaaaagatt				1985
Gln	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu					
	615					620					625					
tcgcttctcg	acg															1998

&lt;210&gt; 426

&lt;211&gt; 625

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 426

Met Arg Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser  
 1 5 10 15

Arg Asp Tyr Phe Ala Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu  
 20 25 30

Glu Tyr Arg Gly Tyr Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly  
 35 40 45

Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala  
 50 55 60

Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His  
 65 70 75 80

Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro  
 85 90 95

His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile  
 100 105 110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn  
 115 120 125

Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu  
 130 135 140

Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu  
 145 150 155 160

Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala  
 165 170 175

Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val  
 180 185 190

Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly  
 195 200 205

Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val  
 210 215 220

Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser  
 225 230 235 240

Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala  
 245 250 255

Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln  
 260 265 270

Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly  
 275 280 285

Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser  
 290 295 300  
 Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly  
 305 310 315 320  
 Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu  
 325 330 335  
 Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu  
 340 345 350  
 Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr  
 355 360 365  
 Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala  
 370 375 380  
 Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser  
 385 390 395 400  
 Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala  
 405 410 415  
 Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala  
 420 425 430  
 Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp  
 435 440 445  
 Ser Leu Arg Glu Met Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu  
 450 455 460  
 Glu Gln Ile Lys Lys Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val  
 465 470 475 480  
 Leu Phe Leu Gly Arg His Val Gly Phe Pro Val Ala Leu Glu Gly Ala  
 485 490 495  
 Leu Lys Leu Lys Glu Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala  
 500 505 510  
 Gly Glu Leu Lys His Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro  
 515 520 525  
 Ile Phe Val Ile Val Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser  
 530 535 540  
 Lys Val Val Ser Asn Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr  
 545 550 555 560  
 Ile Val Ile Ala Glu Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn  
 565 570 575  
 Phe Ile Ile Arg Ile Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu  
 580 585 590  
 Ser Thr Val Pro Leu Gln Ile Phe Ala Cys Ala Val Ala Thr Ala Lys  
 595 600 605  
 Gly Tyr Asn Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val

610

615

620

Glu  
625

&lt;210&gt; 427

&lt;211&gt; 666

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(666)

&lt;223&gt; RXN03179

&lt;400&gt; 427

gct	cgt	gag	gca	tgg	cgc	att	ttc	atg	tcc	cac	tgg	gat	ctc	tac	gca	48
Ala	Arg	Glu	Ala	Trp	Arg	Ile	Phe	Met	Ser	His	Trp	Asp	Leu	Tyr	Ala	
1				5					10					15		

gga	acc	gca	act	ggc	tac	tgg	gtg	gag	cag	gaa	ttt	gag	cac	ggt	ttc	96
Gly	Thr	Ala	Thr	Gly	Tyr	Trp	Val	Glu	Gln	Glu	Phe	Glu	His	Val	Phe	
			20				25						30			

ggc	atc	aac	gcg	gag	cgc	ctg	aat	gtt	ggc	acc	cca	gaa	cat	gct	gac	144
Gly	Ile	Asn	Ala	Glu	Arg	Leu	Asn	Val	Gly	Thr	Pro	Glu	His	Ala	Asp	
		35				40						45				

gcc	atc	ttt	gat	gag	ctg	acc	gat	att	ctt	gcc	aag	cca	gat	ttc	cga	192
Ala	Ile	Phe	Asp	Glu	Leu	Thr	Asp	Ile	Leu	Ala	Lys	Pro	Asp	Phe	Arg	
	50					55					60					

cca	cgc	gca	ctg	gct	gag	cag	ttc	aac	ttg	gaa	gtt	cta	gcc	acc	acc	240
Pro	Arg	Ala	Leu	Ala	Glu	Gln	Phe	Asn	Leu	Glu	Val	Leu	Ala	Thr	Thr	
65					70					75				80		

gac	gat	ccg	ctc	gat	gac	ctg	gca	gat	cac	aag	gca	ctg	gca	gat	gat	288
Asp	Asp	Pro	Leu	Asp	Asp	Leu	Ala	Asp	His	Lys	Ala	Leu	Ala	Asp	Asp	
			85						90					95		

cca	acc	ttc	tcc	cct	cgt	gtg	ctc	cct	acc	ttc	cgc	cca	gac	gca	tac	336
Pro	Thr	Phe	Ser	Pro	Arg	Val	Leu	Pro	Thr	Phe	Arg	Pro	Asp	Ala	Tyr	
			100					105						110		

acc	aag	atg	tac	aac	gct	ggt	tgg	gca	gaa	aaa	acc	acc	aag	ctt	atc	384
Thr	Lys	Met	Tyr	Asn	Ala	Gly	Trp	Ala	Glu	Lys	Thr	Thr	Lys	Leu	Ile	
		115					120						125			

gat	acc	gca	ggt	gac	ggc	aag	gca	ggc	tgg	gag	ggt	tac	ctt	cag	gca	432
Asp	Thr	Ala	Gly	Asp	Gly	Lys	Ala	Gly	Trp	Glu	Gly	Tyr	Leu	Gln	Ala	
	130					135					140					

atg	cgc	aac	cgc	cgc	cag	tac	ttc	atc	aat	cac	ggt	gca	acc	tcc	gcg	480
Met	Arg	Asn	Arg	Arg	Gln	Tyr	Phe	Ile	Asn	His	Gly	Ala	Thr	Ser	Ala	
145					150					155				160		

gac	cac	ggt	ctc	cac	gac	acc	gac	acc	acc	cca	ctg	agc	cac	aaa	gat	528
Asp	His	Gly	Leu	His	Asp	Thr	Asp	Thr	Thr	Pro	Leu	Ser	His	Lys	Asp	
			165						170					175		



gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576  
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
                   180                  185                  190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt tcg cgg aaa tgt 624  
 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys  
                   195                  200                  205

cca aga aga cgg ctg gtc atg acc atc cac cag gtg tgt acc 666  
 Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr  
                   210                  215                  220

<210> 428

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala  
   1                  5                  10                  15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe  
                   20                  25                  30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp  
                   35                  40                  45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg  
                   50                  55                  60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr  
                   65                  70                  75                  80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp  
                   85                  90                  95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr  
                   100                  105                  110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile  
                   115                  120                  125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala  
                   130                  135                  140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala  
                   145                  150                  155                  160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp  
                   165                  170                  175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
                   180                  185                  190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys  
                   195                  200                  205

Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr  
                   210                  215                  220

<210> 429  
 <211> 672  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(672)  
 <223> FRXA02872

<400> 429

gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca	48
Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala	
1 5 10 15	
gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc	96
Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe	
20 25 30	
ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac	144
Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp	
35 40 45	
gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga	192
Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg	
50 55 60	
cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc	240
Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr	
65 70 75 80	
gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat	288
Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp	
85 90 95	
cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac	336
Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr	
100 105 110	
acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc	384
Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile	
115 120 125	
gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca	432
Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala	
130 135 140	
atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg	480
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala	
145 150 155 160	
gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat	528
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp	
165 170 175	
gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct	576
Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala	
180 185 190	
gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt ttc gcg gaa atg	624

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met  
 195 200 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc 672  
 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg  
 210 215 220

<210> 430

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala  
 1 5 10 15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe  
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp  
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg  
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr  
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp  
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr  
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile  
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala  
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala  
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp  
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met  
 195 200 205

Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg  
 210 215 220

<210> 431

<211> 533  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(510)  
 <223> RXN03180

<400> 431

ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg	48
Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp	
1 5 10 15	
ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca	96
Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala	
20 25 30	
gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc	144
Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg	
35 40 45	
gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac	192
Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn	
50 55 60	
ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc	240
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe	
65 70 75 80	
att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga	288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly	
85 90 95	
ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc	336
Leu Ser Glu Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu	
100 105 110	
cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat	384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp	
115 120 125	
gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa	432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln	
130 135 140	
atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac	480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His	
145 150 155 160	
gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga	530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln	
165 170	
tgt	533

<210> 432  
 <211> 170  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 432

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp  
 1 5 10 15  
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala  
 20 25 30  
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg  
 35 40 45  
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn  
 50 55 60  
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe  
 65 70 75 80  
 Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly  
 85 90 95  
 Leu Ser Glu Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu  
 100 105 110  
 Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp  
 115 120 125  
 Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln  
 130 135 140  
 Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His  
 145 150 155 160  
 Val Arg Ile Ile Pro Asn Gly Lys Asp Gln  
 165 170

&lt;210&gt; 433

&lt;211&gt; 533

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(510)

&lt;223&gt; FRXA02873

&lt;400&gt; 433

ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48  
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp  
 1 5 10 15  
 ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96  
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala  
 20 25 30  
 gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144  
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg  
 35 40 45  
 gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192  
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn

50 55 60  
 ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc 240  
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe  
 65 70 75 80  
 att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga 288  
 Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly  
 85 90 95  
 ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc 336  
 Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu  
 100 105 110  
 cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat 384  
 Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp  
 115 120 125  
 gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa 432  
 Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln  
 130 135 140  
 atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac 480  
 Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His  
 145 150 155 160  
 gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga 530  
 Val Arg Ile Ile Pro Asn Gly Lys Asp Gln  
 165 170  
 tgt 533  
  
 <210> 434  
 <211> 170  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 434  
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp  
 1 5 10 15  
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala  
 20 25 30  
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg  
 35 40 45  
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn  
 50 55 60  
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe  
 65 70 75 80  
 Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly  
 85 90 95  
 Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu  
 100 105 110  
 Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp

115	120	125
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln		
130	135	140
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His		
145	150	155
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln		
165	170	

&lt;210&gt; 435

&lt;211&gt; 798

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(775)

&lt;223&gt; RXA02292

&lt;400&gt; 435

tgcaccacgc cagctgcaac cctgcgcggt ggtctgggaa gttgggtggag gggatcgctcg 60  
 aaaagcgtag gcactaaagt tctcctgcac aatggaggat atg gac aat gac ttt 115  
 Met Asp Asn Asp Phe 5

gaa tct atc gag aaa atg agc agc ggc gat tgg tac gtg gct acc ggc 163  
 Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp Tyr Val Ala Thr Gly  
 10 15 20

gcg gaa cgt gaa gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa 211  
 Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu  
 25 30 35

tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta 259  
 Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu  
 40 45 50

aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca 307  
 Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro  
 55 60 65

gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc 355  
 Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile Gly Glu His Val Phe  
 70 75 80 85

atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg 403  
 Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly  
 90 95 100

gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac 451  
 Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His  
 105 110 115

ccg gtc gat gac tgg gaa atg cgc tcc ggt ggg tgg gaa aat ggc gca 499  
 Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly Trp Glu Asn Gly Ala  
 120 125 130

ccc att tcc att ggc gag gat acg tgg ctg ggt gga aat gtc acc gtc 547  
 Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val  
 135 140 145  
  
 gtt ggt ggc gtg agc att ggc gat agg tgt gtg att ggc gcg ggg ccc 595  
 Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val Ile Gly Ala Gly Pro  
 150 155 160 165  
  
 gtg gtg acc aag gat att ccg gat gat tct att gct gtg ggc aac cct 643  
 Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro  
 170 175 180  
  
 gcg cga gta gtg cgg aaa cgt gat gat agc cgg ctc gaa cgt tcg cag 691  
 Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg Leu Glu Arg Ser Gln  
 185 190 195  
  
 ctg cca gaa ggt gct tcc gtg gat gcg ttg ggg att ctt cct aca aaa 739  
 Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly Ile Leu Pro Thr Lys  
 200 205 210  
  
 tca cct agg ctg tca gaa aat att gcc gaa aaa tat taaatacgca 785  
 Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys Tyr  
 215 220 225  
  
 ggcaactaaga aga 798

<210> 436  
 <211> 225  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 436  
 Met Asp Asn Asp Phe Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp  
 1 5 10 15  
  
 Tyr Val Ala Thr Gly Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala  
 20 25 30  
  
 Leu Leu Phe His Glu Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg  
 35 40 45  
  
 Thr Ala Glu Ile Leu Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys  
 50 55 60  
  
 Thr Ile Lys Ala Pro Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile  
 65 70 75 80  
  
 Gly Glu His Val Phe Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala  
 85 90 95  
  
 Pro Val Arg Ile Gly Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu  
 100 105 110  
  
 Phe Thr Ala Gly His Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly  
 115 120 125  
  
 Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly  
 130 135 140  
  
 Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val



145		150		155		160
Ile Gly Ala Gly Pro Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile						
		165		170		175
Ala Val Gly Asn Pro Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg						
		180		185		190
Leu Glu Arg Ser Gln Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly						
		195		200		205
Ile Leu Pro Thr Lys Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys						
		210		215		220
Tyr						
225						

<210> 437  
 <211> 891  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(868)  
 <223> RXA02666

<400> 437  
 gctcggcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60  
 tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115  
 Met Ser Ser Thr Arg  
 1 5  
 atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163  
 Ile Pro Val Ile Ala Leu Leu Ala Ala Gly Arg Gly Thr Arg Leu  
 10 15 20  
 ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211  
 Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu  
 25 30 35  
 tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259  
 Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu  
 40 45 50  
 atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307  
 Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu  
 55 60 65  
 ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355  
 Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg  
 70 75 80 85  
 ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt 403  
 Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu  
 90 95 100  
 cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc 451  
 Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile

105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg			499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val			
120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca			547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro			
135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc			595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val			
150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc			643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly			
	170	175	180
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac			691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp			
	185	190	195
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg			739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp			
	200	205	210
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa			787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys			
	215	220	225
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa			835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu			
	230	235	240
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg			888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp			
	250	255	
tag			891

&lt;210&gt; 438

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 438

Met	Ser	Ser	Thr	Arg	Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly
1				5					10					15	

Arg	Gly	Thr	Arg	Leu	Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu
			20					25					30		

Arg	Glu	Arg	Thr	Leu	Leu	Glu	Arg	Ser	Leu	Gln	Ala	Met	Leu	Thr	Ser
			35				40					45			

Glu	Ser	Val	Asp	Glu	Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr
		50				55					60				

Tyr	Ala	Arg	Asp	Leu	Leu	Arg	Lys	Arg	Gly	Leu	Leu	Asn	Asp	Pro	Glu
	65					70				75					80

```
<210> 439
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum
```

```

<400> 439
ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60

aaacaaaacc tctaagtaat tcttgaaagg aaattttcac atg tac gct cgt aaa 115
                                         Met Tyr Ala Arg Lys
                                         1                               5

ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala
                        10                        15                        20

tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat 211
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp

```

25	30	35	
ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val 40 45 50			259
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr 55 60 65			307
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln 70 75 80 85			355
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro 90 95 100			403
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala 105 110 115			451
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val 120 125 130			499
gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala 135 140 145			547
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu 150 155 160 165			595
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe 170 175 180			643
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln 185 190 195			691
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu 200 205 210			739
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu 215 220 225			787
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp 230 235 240 245			835
gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val 250 255 260			883
gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu 265 270 275			931

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979  
 Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp  
           280                          285                          290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027  
 Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn  
           295                          300                          305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065  
 Val Ala Asp Phe Lys  
 310

<210> 440

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala  
   1                          5                          10                          15

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp  
           20                          25                          30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr  
           35                          40                          45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp  
           50                          55                          60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala  
           65                          70                          75                          80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val  
           85                          90                          95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu  
           100                          105                          110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser  
           115                          120                          125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly  
           130                          135                          140

Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly  
           145                          150                          155                          160

Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp  
           165                          170                          175

Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser  
           180                          185                          190

Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp  
           195                          200                          205

Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe  
           210                          215                          220

Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala  
225 230 235 240

Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp  
245 250 255

Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln  
260 265 270

Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu  
275 280 285

Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr  
290 295 300

Val Lys Leu Asp Asn Val Ala Asp Phe Lys  
305 310

<210> 441

<211> 963

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(940)

<223> RXA02440

<400> 441

gctgttaatc acgggttggt cagctaccgg gggagcacca cgggcaacag atggggcatc 60

aggcggagga accgtcgata cgctcgggtt ggttgctcgcg atg gtg agc cac ggc 115  
Met Val Ser His Gly  
1 5

gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac 163  
Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp  
10 15 20

gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa 211  
Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu  
25 30 35

atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc 259  
Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val  
40 45 50

gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc 307  
Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val  
55 60 65

gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct 355  
Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala  
70 75 80 85

gga atg aac gaa tac caa gat tat gga atg aca gga ttc ttt ggt caa 403  
Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr Gly Phe Phe Gly Gln  
90 95 100

gat gaa tcc gtc gca gga gca tcc gca gga gcg cgc ctt gcc gag gaa 451  
Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala Arg Leu Ala Glu Glu  
105 110 115

aac gca caa aaa gtt ttg tgt gtg atc cat gaa cag ggc aac tcc tcc 499  
Asn Ala Gln Lys Val Leu Cys Val Ile His Glu Gln Gly Asn Ser Ser  
120 125 130

cag gaa gct cgc tgt ggt ggc gtg tct gaa ggt ttg ggc aaa caa gta 547  
Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly Leu Gly Lys Gln Val  
135 140 145

gaa acc ctg tat gtc aac ggc atg gat ctc acc tca gtg aac tcc acc 595  
Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr Ser Val Asn Ser Thr  
150 155 160 165

ctg cag gca aaa ctt gct caa gac cgc agc att gat tgg gtt gtg gga 643  
Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile Asp Trp Val Val Gly  
170 175 180

ctc cag gct ggt gta tca atg gct att tct gat gcg gca gac gct gcg 691  
Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp Ala Ala Asp Ala Ala  
185 190 195

aac tca gaa gta aag atc gcc acc ttt gat aca aac gca cag ctc atg 739  
Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr Asn Ala Gln Leu Met  
200 205 210

acc gct att cgt gat ggc aag atc caa ttc gcc att gat cag caa cca 787  
Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala Ile Asp Gln Gln Pro  
215 220 225

tat ctg cag ggc tac atg gcc gtg gat tcg ctg tgg ttg gcg cac cga 835  
Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu Trp Leu Ala His Arg  
230 235 240 245

aac ggc acc act gtt ggt ggc gga cga ccc gtg tac aca gga cca gcc 883  
Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val Tyr Thr Gly Pro Ala  
250 255 260

att gtg gat gcc acc aac gtt gat gtc att gct gaa gcc gtt ggg gag 931  
Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala Glu Ala Val Gly Glu  
265 270 275

ggt ctg cga tgacaaaaat caagagtggg gag 963  
Gly Leu Arg  
280

&lt;210&gt; 442

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 442

Met Val Ser His Gly Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg  
1 5 10 15

Lys Gly Ala Glu Asp Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr  
20 25 30

```
<210> 443
<211> 1482
<212> DNA
<213> Corynebacterium glutamicum
```

<400> 443  
aaggcctaga gcagaccatc gattggtacc qcqaaaacga qgcctggtgg cgccctqcca 60



agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa	115
Met Glu Tyr Gly Lys	
1 5	
caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat	163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp	
10 15 20	
ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag	211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln	
25 30 35	
cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa	259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln	
40 45 50	
aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac	307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His	
55 60 65	
gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc	355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe	
70 75 80 85	
gga gct tgg gtg gat ctg cgc gcg ggc tgc agc acg tac ggt aac gtc	403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val	
90 95 100	
gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt	451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly	
105 110 115	
gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac	499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr	
120 125 130	
ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac	547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn	
135 140 145	
ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa	595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys	
150 155 160 165	
gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc	643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg	
170 175 180	
aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc	691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg	
185 190 195	
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc	739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile	
200 205 210	
acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc	787
Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile	
215 220 225	

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc	835
Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg	
230 235 240 245	
gca gca gcg tgg gac atc aac gca gcg gca gtg gct aac ctc gcg acc	883
Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val Ala Asn Leu Ala Thr	
250 255 260	
atc gcg cgc gac aac aac ctc acc ctc gtg cac gtg tcc tca gat tat	931
Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His Val Ser Ser Asp Tyr	
265 270 275	
gtc ttc gac ggt gcg gcc gaa tcc tac gat gaa aac gca ccg ttt tcc	979
Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu Asn Ala Pro Phe Ser	
280 285 290	
cca ctc ggc gtg tac ggc caa tcc aaa gca gcc ggc gac atc gga gac	1027
Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala Gly Asp Ile Gly Asp	
295 300 305	
acc acc gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc	1075
Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly	
310 315 320 325	
gat ggc aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc	1123
Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly	
330 335 340	
atc gca cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc	1171
Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr	
345 350 355	
gaa gac atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca	1219
Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala	
360 365 370	
tat ggc acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc	1267
Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala	
375 380 385	
gat gtt gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg	1315
Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val	
390 395 400 405	
agc acc gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg	1363
Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu	
410 415 420	
aac tcc gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca	1411
Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala	
425 430 435	
ccg acc tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag	1459
Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys	
440 445 450	
tgaaaggcat catcctcgca ggt	1482

&lt;210&gt; 444

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 444

```

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly
 1          5          10          15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
      20          25          30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
      35          40          45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
      50          55          60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
      65          70          75          80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
      85          90          95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
      100          105          110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
      115          120          125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
      130          135          140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
      145          150          155          160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
      165          170          175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
      180          185          190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
      195          200          205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
      210          215          220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
      225          230          235          240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
      245          250          255

Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His
      260          265          270

Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu
      275          280          285

Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala
      290          295          300

```

Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr  
 305 310 315 320  
 Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser  
 325 330 335  
 Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly  
 340 345 350  
 Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu  
 355 360 365  
 Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu  
 370 375 380  
 Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr  
 385 390 395 400  
 Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala  
 405 410 415  
 Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala  
 420 425 430  
 Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu  
 435 440 445  
 Lys Glu Leu Ser Lys  
 450

&lt;210&gt; 445

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(426)

&lt;223&gt; FRXA01569

&lt;400&gt; 445

gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc gat ggc 48  
 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly  
 1 5 10 15  
 aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca 96  
 Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala  
 20 25 30  
 cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac 144  
 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp  
 35 40 45  
 atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca tat ggc 192  
 Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly  
 50 55 60  
 acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc gat gtt 240  
 Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val  
 65 70 75 80

gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg agc acc 288  
 Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr  
                     85                    90                    95

gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg aac tcc 336  
 Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser  
                     100                    105                    110

gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca ccg acc 384  
 Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr  
                     115                    120                    125

tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 426  
 Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys  
                     130                    135                    140

tgaaaggcat catcctcgca ggt 449

<210> 446

<211> 142

<212> PRT

<213> Corynebacterium glutamicum.

<400> 446

Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly  
                     1                    5                    10                    15

Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala  
                     20                    25                    30

Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp  
                     35                    40                    45

Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly  
                     50                    55                    60

Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val  
                     65                    70                    75                    80

Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr  
                     85                    90                    95

Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser  
                     100                    105                    110

Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr  
                     115                    120                    125

Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys  
                     130                    135                    140

<210> 447

<211> 1028

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

&lt;222&gt; (101)..(1021)

&lt;223&gt; FRXA02055

&lt;400&gt; 447

```

aaggcctaga gcagaccatc gattggtacc gcgaaaacga ggcctggtgg cgccctgccca 60

agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
                                         Met Glu Tyr Gly Lys
                                         1                               5

caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
                        10                        15                        20

ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
                        25                        30                        35

cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
                        40                        45                        50

aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
                        55                        60                        65

gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
                        70                        75                        80                        85

gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc 403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
                        90                        95                        100

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt 451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
                        105                        110                        115

gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac 499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
                        120                        125                        130

ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac 547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
                        135                        140                        145

ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa 595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
                        150                        155                        160                        165

gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc 643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
                        170                        175                        180

aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc 691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
                        185                        190                        195

gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc 739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile
                        200                        205                        210

```

acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc 787  
 Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile  
 215 220 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc 835  
 Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg  
 230 235 240 245

gca gca gcg tgg gac att aac gca gcg gca gtg gct acc tcg cga cca 883  
 Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Thr Ser Arg Pro  
 250 255 260

tcg cgc gcg aca aca acc tca ccc tcg tgc acg tgt cct cag att atg 931  
 Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met  
 265 270 275

tct tcg acg gtg cgg gcg aat cct acg atg aaa acg cac cgt ttt ccc 979  
 Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro  
 280 285 290

cac tcg gcg tgt acg gcc aat cca aag cag ccg gcg aca tcg 1021  
 His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro Ala Thr Ser  
 295 300 305

taagcac 1028

&lt;210&gt; 448

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 448

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly  
 1 5 10 15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe  
 20 25 30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp  
 35 40 45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr  
 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala  
 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser  
 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val  
 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly  
 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His  
 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr  
 145 150 155 160  
 Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr  
 165 170 175  
 Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu  
 180 185 190  
 Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg  
 195 200 205  
 Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys  
 210 215 220  
 Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln  
 225 230 235 240  
 Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val  
 245 250 255  
 Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr  
 260 265 270  
 Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys  
 275 280 285  
 Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro  
 290 295 300  
 Ala Thr Ser  
 305

<210> 449  
 <211> 1056  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1033)  
 <223> RXA00825

<400> 449  
 cccgttcacg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60  
 tagtgcaacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt 115  
 Met Arg Thr Val Val  
 1 5  
 acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163  
 Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile  
 10 15 20  
 aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211  
 Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg  
 25 30 35  
 ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg 259  
 Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val



40	45	50	
gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His 55 60 65			307
aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His 70 75 80 85			355
tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr 90 95 100			403
atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val 105 110 115			451
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro 120 125 130			499
gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser 135 140 145			547
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly 150 155 160 165			595
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln 170 175 180			643
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu 185 190 195			691
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg 200 205 210			739
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser 215 220 225			787
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu 230 235 240 245			835
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser 250 255 260			883
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg 265 270 275			931
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro 280 285 290			979

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc 1027  
 Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg  
 295 300 305

act cac taggggaaaa tccaccacaa atc 1056  
 Thr His  
 310

<210> 450

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu  
 1 5 10 15

Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn  
 20 25 30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly  
 35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu  
 50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln  
 65 70 75 80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr  
 85 90 95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly  
 100 105 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu  
 115 120 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser  
 130 135 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe  
 145 150 155 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val  
 165 170 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile  
 180 185 190

Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp  
 195 200 205

Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala  
 210 215 220

Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile  
 225 230 235 240

Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala  
 245 250 255

Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu  
 260 265 270

Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val  
 275 280 285

Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr  
 290 295 300

Val Glu Tyr Phe Arg Thr His  
 305 310

<210> 451  
 <211> 1140  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1117)  
 <223> RXA02054

<400> 451  
 cctaataaac agccggagca ccctggctgt ttgcagaata ggccgcatcga caacagctac 60

taactctgcc agctcgcccg gacgaactaa ggtagacggc atg act tct ttg ctt 115  
 Met Thr Ser Leu Leu  
 1 5

gtg acc gga ggt gcc gga ttt atc ggc gcc aac ttc gtc cgc caa acc 163  
 Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn Phe Val Arg Gln Thr  
 10 15 20

gta gag cag cac cct gaa tac acc cac atc acg gtg ctg gat aaa ctc 211  
 Val Glu Gln His Pro Glu Tyr Thr His Ile Thr Val Leu Asp Lys Leu  
 25 30 35

acc tac gca gga aac gcc gac aat ctc aaa ggc ctc ccc gac agc aaa 259  
 Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly Leu Pro Asp Ser Lys  
 40 45 50

gta acc ctc atc gaa ggc gat atc tgc gat gct gaa tta gtc gac tcc 307  
 Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala Glu Leu Val Asp Ser  
 55 60 65

ctg gtc aaa gac cac gac atc aca gtc cac ttc gca gca gaa tcc cac 355  
 Leu Val Lys Asp His Asp Ile Thr Val His Phe Ala Ala Glu Ser His  
 70 75 80 85

aac gac aac tcc ctc aac gac ccc tcc ccg ttt gtt cac act aac ctc 403  
 Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe Val His Thr Asn Leu  
 90 95 100

atc ggc acc ttt gtc ctg cta gaa gca gtc cgc aag cac aac aaa cgc 451  
 Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg Lys His Asn Lys Arg  
 105 110 115

ttc cac cac atc tcc acc gat gaa gtc ttc ggc gat cta gag ctg gat 499  
 Phe His His Ile Ser Thr Asp Glu Val Phe Gly Asp Leu Glu Leu Asp  
 120 125 130

gat cca aac cgc ttc act gaa acc acc gcc tac aag cca tcg tct cca 547  
 Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr Lys Pro Ser Ser Pro  
 135 140 145

tat tct gca acc aag gca ggg tct gat cac ttg gta cac gca tgg atc 595  
 Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu Val His Ala Trp Ile  
 150 155 160 165

cgc tcc ttc gga atc cag gca acc atg tct aac tgc tcc aac aat tac 643  
 Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn Cys Ser Asn Asn Tyr  
 170 175 180

ggt ccc tac cag cac att gaa aag ttc atc ccc cgc cag atc acc aat 691  
 Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro Arg Gln Ile Thr Asn  
 185 190 195

att ctg gcc ggc ctg aca cca aaa ctt tat gga acc ggc gag cag gtc 739  
 Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly Thr Gly Glu Gln Val  
 200 205 210

cgc gac tgg atc cac gtc gat gat cac aat gac gcc gtc cac ctg atc 787  
 Arg Asp Trp Ile His Val Asp Asp His Asn Asp Ala Val His Leu Ile  
 215 220 225

ctg agt aag ggc aag atc ggc gaa acc tac atc atc ggc gcc gac aac 835  
 Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile Ile Gly Ala Asp Asn  
 230 235 240 245

gat cat gtg aat aac aag cag gtc atc gag ctt att tgt gaa ctc atg 883  
 Asp His Val Asn Asn Lys Gln Val Ile Glu Leu Ile Cys Glu Leu Met  
 250 255 260

ggc ctc gac aaa aac gca tac gag cac gtc gca gac cgc ccc ggc cac 931  
 Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala Asp Arg Pro Gly His  
 265 270 275

gat atg cgt tac gcc atg gat tcc acc aag ctg cgc acc gag ctc ggc 979  
 Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu Arg Thr Glu Leu Gly  
 280 285 290

tgg gca cct aaa tac acc gac gtt gat tcc ggc atg cgc aaa ggc cta 1027  
 Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly Met Arg Lys Gly Leu  
 295 300 305

gag cag acc atc gat tgg tac cgc gaa aac gag gcc tgg tgg cgc cct 1075  
 Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu Ala Trp Trp Arg Pro  
 310 315 320 325

gcc aag aac aac gtc gaa gct acc tac gct aag cag gga caa 1117  
 Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys Gln Gly Gln  
 330 335

taatggaata cggtaaaciaa ctc 1140

&lt;210&gt; 452

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 452

```

Met Thr Ser Leu Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn
 1           5           10           15

Phe Val Arg Gln Thr Val Glu Gln His Pro Glu Tyr Thr His Ile Thr
      20           25           30

Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly
      35           40           45

Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala
      50           55           60

Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe
      65           70           75           80

Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe
      85           90           95

Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg
      100          105          110

Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly
      115          120          125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr
      130          135          140

Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu
      145          150          155          160

Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn
      165          170          175

Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro
      180          185          190

Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly
      195          200          205

Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp
      210          215          220

Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile
      225          230          235          240

Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu
      245          250          255

Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala
      260          265          270

Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu
      275          280          285

Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly
      290          295          300

```

<400> 453																
gcggtcattg tgaccacaaa tcgtgtggaa ttgctgcggc attccctcga ggttgttgcc																60
aatcaaacct atccggtgaa acacattgtg gtggtggata atg ggg cgg atc cta																115
Met Gly Arg Ile Leu																
1 5																
gta ttc tat agt gtc act tta gag gtg gcg gga gac cgt ccc gtt tac																163
Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly Asp Arg Pro Val Tyr																
10 15 20																
acg cct tcg cgc acc aat ttg ggc gac ggt ggc ggt ttt gct ttt ggt																211
Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly Gly Phe Ala Phe Gly																
25 30 35																
ttt ttg acg gcg ttg gcg ctg ggg gcg aac gcg gtg tgg tgc aca gac																259
Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala Val Trp Cys Thr Asp																
40 45 50																
gat gac ggc cgg ccg gag ggg cca ggg gtg ttg aag acg ctt atc gac																307
Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu Lys Thr Leu Ile Asp																
55 60 65																
gcc gct tct cgg cat aat ctg gag gag gtt tct ccg gtg gta tgc aat																355
Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser Pro Val Val Cys Asn																
70 75 80 85																
gct gat gat ccg gag cgg ttg gca ttt ccg ctg cgt cgg ggc ttg gag																403
Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu Arg Arg Gly Leu Glu																
90 95 100																
tgg cgt cgg atg cgc agt gag ttg att gat cca gcc aac ccg gag gat																451
Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro Ala Asn Pro Glu Asp																
105 110 115																
gat ttg ctg ccg ggc atc gcc tcc ttg ttc aat ggt gcc ctg atc agc																499
Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser																
120 125 130																
gct tat gca atg gag cgc att ggc gtg ccg gac tat cga ctg ttt att																547
Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile																

135	140	145	
cgc ggc gat gag gtg gag tat cac cgc cgt ttg gtg cgt tcc ggt ttg			595
Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu			
150	155	160	165
ccg .ttt ggt acg tgt ttg acc acg gcg tat ttg cac ccg gat ggt tct			643
Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser			
	170	175	180
gat gag ttc aag ccg att ctg ggt ggg cgg atg cat acg cag tat ccg			691
Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro			
	185	190	195
gat aat gat ttc aag agg ttt ttc acc tac cgc aac cgt ggc tac ctg			739
Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu			
	200	205	210
atg agc cag ccg gga atg cgc aag ctt ctc cct cag gaa tat gcg cgc			787
Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg			
	215	220	225
ttt gcg tgg ttc ttc ctg gtt cag aaa cgg gat gtg aag gga ttc cgg			835
Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg			
230	235	240	245
gag tgg ctg cgc ctg cac aaa ctg ggc cgc gac gag aaa ttc aat agg			883
Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg			
	250	255	260
ccc tagatcagtt ttagtagttc ctc			909
Pro			

<210> 454  
 <211> 262  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 454  
 Met Gly Arg Ile Leu Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly  
 1 5 10 15  
 Asp Arg Pro Val Tyr Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly  
 20 25 30  
 Gly Phe Ala Phe Gly Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala  
 35 40 45  
 Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu  
 50 55 60  
 Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser  
 65 70 75 80  
 Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu  
 85 90 95  
 Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro  
 100 105 110

Ala Asn Pro Glu Asp Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn  
 115 120 125

Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp  
 130 135 140

Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu  
 145 150 155 160

Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu  
 165 170 175

His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met  
 180 185 190

His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg  
 195 200 205

Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro  
 210 215 220

Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp  
 225 230 235 240

Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp  
 245 250 255

Glu Lys Phe Asn Arg Pro  
 260

&lt;210&gt; 455

&lt;211&gt; 555

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(532)

&lt;223&gt; FRXA00427

&lt;400&gt; 455

tgctgatgat ccggagcggg tggcatttcc gctgcgctcg ggcttggagt ggcgtcggat 60

gcgcagtgag ttgattgata cagccaaccc ggaggatgat ttg ctg ccg ggc atc 115  
 Leu Leu Pro Gly Ile  
 1 5

gcc tcc ttg ttc aat ggt gcc ctg atc agc gct tat gca atg gag cgc 163  
 Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg  
 10 15 20

att ggc gtg ccg gac tat cga ctg ttt att cgc ggc gat gag gtg gag 211  
 Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu  
 25 30 35

tat cac cgc cgt ttg gtg cgt tcc ggt ttg ccg ttt ggt acg tgt ttg 259  
 Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu  
 40 45 50



acc acg gcg tat ttg cac ccg gat ggt tct gat gag ttc aag ccg att 307  
 Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile  
 55 60 65

ctg ggt ggg cgg atg cat acg cag tat ccg gat aat gat ttc aag agg 355  
 Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg  
 70 75 80 85

ttt ttc acc tac cgc aac cgt ggc tac ctg atg agc cag ccg gga atg 403  
 Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met  
 90 95 100

cgc aag ctt ctc cct cag gaa tat gcg cgc ttt gcg tgg ttc ttc ctg 451  
 Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu  
 105 110 115

gtt cag aaa cgg gat gtg aag gga ttc cgg gag tgg ctg cgc ctg cac 499  
 Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His  
 120 125 130

aaa ctg ggc cgc gac gag aaa ttc aat agg ccc tagatcagtt ttagtagttc 552  
 Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro  
 135 140

ctc 555

&lt;210&gt; 456

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 456

Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala  
 1 5 10 15

Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg  
 20 25 30

Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro  
 35 40 45

Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp  
 50 55 60

Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp  
 65 70 75 80

Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met  
 85 90 95

Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe  
 100 105 110

Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu  
 115 120 125

Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro  
 130 135 140

<210> 457  
<211> 507  
<212> DNA  
<213> Corynebacterium glutamicum

```
<220>  
<221> CDS  
<222> (101)..(484)  
<223> RXA00327
```

[illegible]

```
<210> 458
<211> 128
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 458

Met Ile Gln Ala Ala Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg  
 1 5 10 15  
 Leu Ser Asn Pro Leu Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser  
 20 25 30  
 Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys  
 35 40 45  
 Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser  
 50 55 60  
 Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu  
 65 70 75 80  
 Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val  
 85 90 95  
 Ala Trp Leu Gly Leu Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu  
 100 105 110  
 Ala Val Cys Leu Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg  
 115 120 125

<210> 459  
 <211> 615  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(592)  
 <223> RXA00328

<400> 459  
 gtcacgggat ttgtttagc ccgactcaag ggtggaccgg gccgcagatt actcgcccag 60  
 attaggtcta ccaaggactt ttaaagatcg ggtaaaacct gtg ggc gtt gaa agg 115  
 Val Gly Val Glu Arg  
 1 5  
 ggc aag gtc tct gcc aag gca cta gtt gtc tgg ttg acg gca atg tgc 163  
 Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp Leu Thr Ala Met Cys  
 10 15 20  
 gtg tac atc gtg gcc att gct ggt cga aca tca ttt ggt gtc gcc gga 211  
 Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser Phe Gly Val Ala Gly  
 25 30 35  
 gtg cat gcg atc gat cgc ttt gat atc gac gcc tcc cgg ttg gcc gtg 259  
 Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala Ser Arg Leu Ala Val  
 40 45 50  
 ttc act tct gtt cag gtt gga gtc tat gtt ctc gcg cag att ccc atg 307  
 Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu Ala Gln Ile Pro Met  
 55 60 65

ggc atg ctg gtg gac agg ttc gac gcc cgg aaa ctc ttg ctg gct ggc 355  
 Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys Leu Leu Leu Ala Gly  
 70 75 80 85  
 gct tta att ttg gca gct ggc cag ctc att ttg ggt ttc act gat tct 403  
 Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser  
 90 95 100  
 tat atg atc gcc att ttt gcc cga gtg ctc atc agt gtt ggc gat tct 451  
 Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile Ser Val Gly Asp Ser  
 105 110 115  
 tct gca ttt ttg tcc gtg atg cga ctg ttg ccc aac tgg ttc ccg atg 499  
 Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro Asn Trp Phe Pro Met  
 120 125 130  
 tct tgg aca cct gtg ttg cag cag ctc acg ggc gct ttt ggc ttt gtg 547  
 Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly Ala Phe Gly Phe Val  
 135 140 145  
 ggg cag ttt tct ccg cgg tgc cgt ttt tgc aca tac tca aca cct 592  
 Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr Tyr Ser Thr Pro  
 150 155 160  
 taggggtggac aattcctttc gca 615

&lt;210&gt; 460

&lt;211&gt; 164

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 460

Val Gly Val Glu Arg Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp  
 1 5 10 15  
 Leu Thr Ala Met Cys Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser  
 20 25 30  
 Phe Gly Val Ala Gly Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala  
 35 40 45  
 Ser Arg Leu Ala Val Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu  
 50 55 60  
 Ala Gln Ile Pro Met Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys  
 65 70 75 80  
 Leu Leu Leu Ala Gly Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu  
 85 90 95  
 Gly Phe Thr Asp Ser Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile  
 100 105 110  
 Ser Val Gly Asp Ser Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro  
 115 120 125  
 Asn Trp Phe Pro Met Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly  
 130 135 140  
 Ala Phe Gly Phe Val Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr

145

150

155

160

Tyr Ser Thr Pro

&lt;210&gt; 461

&lt;211&gt; 1347

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1324)

&lt;223&gt; RXA00329

&lt;400&gt; 461

tgtgaagaac aatgatcaac ggccttcgcc aagaccgcat cccagagaga aagtaactac 60

ccgcgccctc	atagtttggg	cagcagcctg	tcttgtgtat	atg	gca	gcc	att	acc	115
				Met	Ala	Ala	Ile	Thr	
				1				5	

agc	cgc	acc	agc	ttt	ggt	gtg	gct	gga	gtg	gag	gcc	att	gat	cgt	ttt	163
Ser	Arg	Thr	Ser	Phe	Gly	Val	Ala	Gly	Val	Glu	Ala	Ile	Asp	Arg	Phe	
			10					15					20			

cag	gta	gac	gcc	aca	cgc	att	gca	gta	ttc	act	tct	gtt	cag	gtt	ggt	211
Gln	Val	Asp	Ala	Thr	Arg	Ile	Ala	Val	Phe	Thr	Ser	Val	Gln	Val	Gly	
			25					30					35			

gtg	tac	gcg	ttt	gct	cag	att	ccg	atg	ggc	att	ttg	atc	gat	aag	ttt	259
Val	Tyr	Ala	Phe	Ala	Gln	Ile	Pro	Met	Gly	Ile	Leu	Ile	Asp	Lys	Phe	
		40					45				50					

ggt	cct	cgg	aag	ctc	ctt	gcc	att	ggt	gct	ttg	gtg	atg	ggt	atc	ggc	307
Gly	Pro	Arg	Lys	Leu	Leu	Ala	Ile	Gly	Ala	Leu	Val	Met	Gly	Ile	Gly	
	55					60					65					

cag	ctc	att	ttg	ggc	ttt	acg	gat	agc	tat	tcc	atc	gcg	att	att	gcc	355
Gln	Leu	Ile	Leu	Gly	Phe	Thr	Asp	Ser	Tyr	Ser	Ile	Ala	Ile	Ile	Ala	
	70				75					80					85	

cgc	gtg	ttt	atc	ggc	gcc	ggc	gat	gca	tcg	atc	ttc	ctt	tcg	gtt	atg	403
Arg	Val	Phe	Ile	Gly	Ala	Gly	Asp	Ala	Ser	Ile	Phe	Leu	Ser	Val	Met	
				90					95					100		

cgc	atc	ctg	ccg	ttt	tgg	ttc	cca	ctg	aag	cac	acc	cct	att	ttc	acg	451
Arg	Ile	Leu	Pro	Phe	Trp	Phe	Pro	Leu	Lys	His	Thr	Pro	Ile	Phe	Thr	
			105					110					115			

cag	tta	act	acc	tgc	ctt	ggc	cag	ttg	ggc	cag	ttc	ttt	tct	gcg	gtg	499
Gln	Leu	Thr	Thr	Cys	Leu	Gly	Gln	Leu	Gly	Gln	Phe	Phe	Ser	Ala	Val	
		120				125						130				

cct	ttc	atg	gcg	ttg	ttg	ggt	gcg	cag	ggt	tgg	cct	gtg	gcg	ttt	gtc	547
Pro	Phe	Met	Ala	Leu	Leu	Gly	Ala	Gln	Gly	Trp	Pro	Val	Ala	Phe	Val	
	135					140					145					

agc	ctt	ggt	tcc	gtg	gtg	gca	ctc	att	gcg	atc	gca	gcg	ctg	gtg	gcc	595
Ser	Leu	Gly	Ser	Val	Val	Ala	Leu	Ile	Ala	Ile	Ala	Ala	Leu	Val	Ala	

150	155	160	165	
gtt cgg gat act cca gat cct cag cca aaa cct gtc gaa tca gct cag	643			
Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro Val Glu Ser Ala Gln				
170 175 180				
gaa gca gat aaa cca agc ctg cgc gcg agt ttg aag ttg att gtc cgc	691			
Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu Lys Leu Ile Val Arg				
185 190 195				
aat ccg att acg tgg cag ggt ttc ttc att cac tac gta ttg atg gtg	739			
Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His Tyr Val Leu Met Val				
200 205 210				
tgg cag acc gtg ttc tcc atg atg tgg ggc gtc ccg ctg atg act ttg	787			
Trp Gln Thr Val Phe Ser Met Met Trp Gly Val Pro Leu Met Thr Leu				
215 220 225				
ggc atg gga ctg tct gca acg acg gct ggt ttg gtg ttg agc atc aac	835			
Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu Val Leu Ser Ile Asn				
230 235 240 245				
acg ctg tgc atg gtg gta tcg gcg cca atc atc gga ata att tcc gca	883			
Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala				
250 255 260				
cgc ctt ggg tat cgc cgt gac gtg gtc gcc att gcg ctg tcg ttt gtt	931			
Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile Ala Leu Ser Phe Val				
265 270 275				
caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt	979			
Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly				
280 285 290				
ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg	1027			
Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala				
295 300 305				
gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag	1075			
Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys				
310 315 320 325				
att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca	1123			
Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser				
330 335 340				
tcg atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg	1171			
Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala				
345 350 355				
cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg	1219			
His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala				
360 365 370				
att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga	1267			
Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg				
375 380 385				
ctc aag ggt gga ccg ggc cgc aga tta ctc gcc cag att agg tct acc	1315			
Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr				
390 395 400 405				

aag gac ttt taaagatcgg gtaaaacctg tgg  
Lys Asp Phe

1347

&lt;210&gt; 462

&lt;211&gt; 408

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 462

Met Ala Ala Ile Thr Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu  
1 5 10 15

Ala Ile Asp Arg Phe Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr  
20 25 30

Ser Val Gln Val Gly Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile  
35 40 45

Leu Ile Asp Lys Phe Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu  
50 55 60

Val Met Gly Ile Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser  
65 70 75 80

Ile Ala Ile Ile Ala Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile  
85 90 95

Phe Leu Ser Val Met Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His  
100 105 110

Thr Pro Ile Phe Thr Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln  
115 120 125

Phe Phe Ser Ala Val Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp  
130 135 140

Pro Val Ala Phe Val Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile  
145 150 155 160

Ala Ala Leu Val Ala Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro  
165 170 175

Val Glu Ser Ala Gln Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu  
180 185 190

Lys Leu Ile Val Arg Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His  
195 200 205

Tyr Val Leu Met Val Trp Gln Thr Val Phe Ser Met Met Trp Gly Val  
210 215 220

Pro Leu Met Thr Leu Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu  
225 230 235 240

Val Leu Ser Ile Asn Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile  
245 250 255

Gly Ile Ile Ser Ala Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile

260					265					270						
Ala	Leu	Ser	Phe	Val	Gln	Ser	Ala	Val	Trp	Leu	Val	Phe	Leu	Ala	Ser	
275					280					285						
Asp	Ala	Pro	Arg	Gly	Leu	Met	Ala	Ile	Ile	Leu	Val	Asn	Ile	Val	Met	
290					295					300						
Gly	Leu	Thr	Thr	Ala	Ala	Ser	Gly	Tyr	Gly	Phe	Asp	Thr	Ile	Arg	Glu	
305					310					315					320	
Arg	Leu	Asp	Arg	Lys	Ile	Leu	Ala	Ala	Gly	Thr	Gly	Leu	Ala	Asn	Met	
325					330					335						
Gly	Gly	Phe	Leu	Ser	Ser	Met	Val	Ala	Ala	Gln	Val	Met	Gly	Phe	Leu	
340					345					350						
Leu	Asp	His	Ser	Ala	His	Gly	Ser	Thr	Tyr	Thr	Trp	Val	Asp	Phe	Arg	
355					360					365						
Phe	Gly	Phe	Leu	Ala	Ile	Leu	Val	Thr	Trp	Ala	Val	Gly	Val	Thr	Gly	
370					375					380						
Phe	Val	Val	Ala	Arg	Leu	Lys	Gly	Gly	Pro	Gly	Arg	Arg	Leu	Leu	Ala	
385					390					395					400	
Gln	Ile	Arg	Ser	Thr	Lys	Asp	Phe									
405																

<210> 463  
 <211> 2265  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2242)  
 <223> RXN01554

<400> 463  
 tggcctaaac cttatttgta gttgtcaata aatatgaaat tccttagcaa cttgtttaaa 60  
 tagacgtata aacaagtttg aaaaaggaag gttatccatc ttg aaa aag cat gtg 115  
 Leu Lys Lys His Val  
 1 5  
 acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt 163  
 Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu  
 10 15 20  
 ggt tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca 211  
 Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro  
 25 30 35  
 gct cca gat ctt tct gcg ccg tat aca tgg gtg gaa gag ttt gat tcc 259  
 Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Glu Phe Asp Ser  
 40 45 50  
 gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc 307  
 Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly



55	60	65	
agc gac aaa gtt ctc tat acc gaa gat gct tta agt atc gaa gat ggc Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu Ser Ile Glu Asp Gly 70 75 80 85			355
aag ctc acc atc acc act cag cgc cac tgc gtt gac gaa gac ttc gcg Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val Asp Glu Asp Phe Ala 90 95 100			403
atc agt gat cct gtc aac cgc gga aag ctc aat gac agc acc gcg caa Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn Asp Ser Thr Ala Gln 105 110 115			451
gtt gaa cct tgt gct cca ggt cag ttt gaa aag ttc acc agt gcg cgc Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys Phe Thr Ser Ala Arg 120 125 130			499
atc gtc act ccg aaa att gct cgt gga gag ttc gac ctt tct gtc act Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe Asp Leu Ser Val Thr 135 140 145			547
gca act ctt aac acc ggt ggc gtc gaa ggt gtc cga agt gcc att tgg Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val Arg Ser Ala Ile Trp 150 155 160 165			595
atg caa aac ggt gaa cag gcg tgt tcc tca gca acc aac aat ggc ctc Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu 170 175 180			643
tac gga gaa cta gac ctg gta gag cac ttt tct tac gat ctt cgc tcg Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser Tyr Asp Leu Arg Ser 185 190 195			691
cca tgg tct cca tca aac acc cac ttg ggt tgt gat cct gaa agt gtc Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys Asp Pro Glu Ser Val 200 205 210			739
aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu 215 220 225			787
gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val 230 235 240 245			835
gag tac ttc att gat gat gag gcg att aac cgc cag tca tgg cgc aac Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn 250 255 260			883
gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala 265 270 275			931
cag aag ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn 280 285 290			979
caa aag gta gaa agc gcc gac tgg gca aaa cca cgt tcc tct gag gaa Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro Arg Ser Ser Glu Glu 295 300 305			1027

gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly 310 315 320 325	1075
tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu 330 335 340	1123
ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu 345 350 355	1171
cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser 360 365 370	1219
tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu 375 380 385	1267
caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val 390 395 400 405	1315
acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp Ile Ala Thr Pro Glu 410 415 420	1363
aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser 425 430 435	1411
tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu 440 445 450	1459
acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg 455 460 465	1507
ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp 470 475 480 485	1555
gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg 490 495 500	1603
gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg 505 510 515	1651
cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly 520 525 530	1699
gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe 535 540 545	1747

acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc 1795  
 Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly  
 550 555 560 565

aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag 1843  
 Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys  
 570 575 580

ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt 1891  
 Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu  
 585 590 595

att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca 1939  
 Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr  
 600 605 610

gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac 1987  
 Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp  
 615 620 625

cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct 2035  
 His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro  
 630 635 640 645

gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat 2083  
 Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp  
 650 655 660

gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag 2131  
 Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu  
 665 670 675

acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc 2179  
 Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe  
 680 685 690

aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc 2227  
 Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe  
 695 700 705

atg aga cag ttc aag taatccttgt gggcgctttg tct 2265  
 Met Arg Gln Phe Lys  
 710

&lt;210&gt; 464

&lt;211&gt; 714

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 464

Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe  
 1 5 10 15

Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala  
 20 25 30

Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val  
 35 40 45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg

50	55	60
Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu 65 70 75 80		
Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val 85 90 95		
Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn 100 105 110		
Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys 115 120 125		
Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe 130 135 140		
Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val 145 150 155 160		
Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala 165 170 175		
Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser 180 185 190		
Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys 195 200 205		
Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys 210 215 220		
Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr 225 230 235 240		
Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg 245 250 255		
Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp 260 265 270		
Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp 275 280 285		
Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro 290 295 300		
Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg 305 310 315 320		
Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro 325 330 335		
Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg 340 345 350		
Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp 355 360 365		
Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln 370 375 380		

Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly  
 385 390 395 400  
 Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp  
 405 410 415  
 Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu  
 420 425 430  
 Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala  
 435 440 445  
 Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu  
 450 455 460  
 Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe  
 465 470 475 480  
 Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu  
 485 490 495  
 Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly  
 500 505 510  
 Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu  
 515 520 525  
 Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp  
 530 535 540  
 Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly  
 545 550 555 560  
 Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg  
 565 570 575  
 Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly  
 580 585 590  
 Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys  
 595 600 605  
 Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His  
 610 615 620  
 Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val  
 625 630 635 640  
 Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly  
 645 650 655  
 Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly  
 660 665 670  
 Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu  
 675 680 685  
 Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn  
 690 695 700

Leu Ile Asn Gln Phe Met Arg Gln Phe Lys  
705 710

<210> 465  
<211> 389  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(382)  
<223> RXN03015

<400> 465  
ccgggtttgc ctgaggtttt ggagcgcaat ctggaaaatg gtcgcctgaa cttcactact 60  
gattatgcgg aggctgcggc ttctgcgcag gtgcatttct ttg ggc gtg ggt act . 115  
Leu Gly Val Gly Thr  
1 5  
cct cag cag aag ggt act tat gcg gcg gat ctg acg tat gtt cgt cag 163  
Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu Thr Tyr Val Arg Gln  
10 15 20  
gtt gtt gag gat ttg gtg ccg ctg ctt gag ggc gag cac att att ttc 211  
Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly Glu His Ile Ile Phe  
25 30 35  
ggc aag tct acg gtt ccg gtt ggt act gct gag cag ttg cag gag ctt 259  
Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu Gln Leu Gln Glu Leu  
40 45 50  
gct gat tct ctg gtc aag cct ggt tcg cac gtg gag atc gcg tgg aat 307  
Ala Asp Ser Leu Val Lys Pro Gly Ser His Val Glu Ile Ala Trp Asn  
55 60 65  
ccg gag ttc ttg cgt gag ggc tac gcg gtc aaa gac acc atc act ccg 355  
Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys Asp Thr Ile Thr Pro  
70 75 80 85  
gac cgc atc gtg gtg ggt gtg cgt gaa taagaca 389  
Asp Arg Ile Val Val Gly Val Arg Glu  
90

<210> 466  
<211> 94  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 466  
Leu Gly Val Gly Thr Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu  
1 5 10 15  
Thr Tyr Val Arg Gln Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly  
20 25 30  
Glu His Ile Ile Phe Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu  
35 40 45

Gln Leu Gln Glu Leu Ala Asp Ser Leu Val Lys Pro Gly Ser His Val  
 50 55 60

Glu Ile Ala Trp Asn Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys  
 65 70 75 80

Asp Thr Ile Thr Pro Asp Arg Ile Val Val Gly Val Arg Glu  
 85 90

<210> 467  
 <211> 801  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(778)  
 <223> RXN03056

<400> 467  
 ttactatcac tggttttgca gatgagatcg cacatgatct cgacgaacag atttccttac 60

ttaataaaact gaagaacagc tcgcggaagc taaagccaaa ttg gat gcc gca gga 115  
 Leu Asp Ala Ala Gly  
 1 5

att tca ctt tca gcc gtt gga tcc gac ttc ggc aag atc aac atc acc 163  
 Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly Lys Ile Asn Ile Thr  
 10 15 20

gat cct ttt gaa gat cac ttg gag cgc gca cgc cac ggt gtt gag gtc 211  
 Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg His Gly Val Glu Val  
 25 30 35

gct aag ctc ttc ggc gcg aaa tac atc cgc atg ttc tcc ttc ttt att 259  
 Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile  
 40 45 50

gca gaa ggc gac aac cct gaa agc ttc cgc aaa gaa gta ctc tcc cgc 307  
 Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys Glu Val Leu Ser Arg  
 55 60 65

acc cac gca atg gtc gaa ctc gca gaa gcc ggc ggc atc acc ctc ctc 355  
 Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu  
 70 75 80 85

cac gaa aat gaa aag gga atc tat ggc gac tcc ccg cag cgc gtg aag 403  
 His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys  
 90 95 100

gat tta atc acc agc atc gac tcc cct aac tac cgc gca atc tac gac 451  
 Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp  
 105 110 115

gca gct aac tac gtg caa acc gga ttc aag cct ttt gat gag gca tgg 499  
 Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp  
 120 125 130

ccg atc gtt aag gac tac gtc gac tac gtc cac atc aag gac gcg acc 547  
 Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His Ile Lys Asp Ala Thr

135                      140                      145  
 att cca gat gca gag cac ccc atc gga atc atc aag cca gca gga caa 595  
 Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile Lys Pro Ala Gly Gln  
 150                      155                      160                      165  
 ggc gac ggc caa tac cca gag ctc ctt gcc gcg cta aac gcc gac ggt 643  
 Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala Leu Asn Ala Asp Gly  
 170                      175                      180  
 tac aac gga ttc gtc tcc atc gag cct cac ctg ggt gac ttc gat gaa 691  
 Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu Gly Asp Phe Asp Glu  
 185                      190                      195  
 ttc ggc gga ctc tgc gga cct gac ctg tgg acc agc gca tgc gac gct 739  
 Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr Ser Ala Cys Asp Ala  
 200                      205                      210  
 ctc gca gga atc ctg aac aac atc aac gcc gag tac aac taaggacaac 788  
 Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu Tyr Asn  
 215                      220                      225  
 tgataatgac aaa 801  
  
 <210> 468  
 <211> 226  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 468  
 Leu Asp Ala Ala Gly Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly  
 1                      5                      10                      15  
 Lys Ile Asn Ile Thr Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg  
 20                      25                      30  
 His Gly Val Glu Val Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met  
 35                      40                      45  
 Phe Ser Phe Phe Ile Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys  
 50                      55                      60  
 Glu Val Leu Ser Arg Thr His Ala Met Val Glu Leu Ala Glu Ala Gly  
 65                      70                      75                      80  
 Gly Ile Thr Leu Leu His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser  
 85                      90                      95  
 Pro Gln Arg Val Lys Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr  
 100                      105                      110  
 Arg Ala Ile Tyr Asp Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro  
 115                      120                      125  
 Phe Asp Glu Ala Trp Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His  
 130                      135                      140  
 Ile Lys Asp Ala Thr Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile  
 145                      150                      155                      160



Lys Pro Ala Gly Gln Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala  
 165 170 175  
 Leu Asn Ala Asp Gly Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu  
 180 185 190  
 Gly Asp Phe Asp Glu Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr  
 195 200 205  
 Ser Ala Cys Asp Ala Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu  
 210 215 220  
 Tyr Asn  
 225

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(664)  
 <223> RXN03030

<400> 469  
 gaagatgaag cagaaaagat cattgggtgcg ccagagggttt ctgcattggg caacaaagca 60

cagcttgatt ccgtcacctt gctgcgtaac aaccccatcc gtg ctg cca ctg gat 115  
 Val Leu Pro Leu Asp  
 1 5

cct gca gca agc ctg aag atc tac cca ttg gtt act ggc cgt acc aag 163  
 Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val Thr Gly Arg Thr Lys  
 10 15 20

atc gac gag gtt caa cta cag ctg gaa gca gcc att cgc gca gaa ctc 211  
 Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala Ile Arg Ala Glu Leu  
 25 30 35

cca ggg gta acc ttg gtg tct tcc gag tca gaa gca gat ctt gca atc 259  
 Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu Ala Asp Leu Ala Ile  
 40 45 50

gtg tgg gct cgc cct gaa att gca ctg ttt gaa gat gac ctc gaa ggt 307  
 Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu Asp Asp Leu Glu Gly  
 55 60 65

gtt tcc ctc tct gtt gac cct cgt gcc aat ggt gtc gat gtg gaa cgc 355  
 Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly Val Asp Val Glu Arg  
 70 75 80 85

gtt cag gct gtg gaa gct gca gtc cca acc atc ttg gct gtg aac ttc 403  
 Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile Leu Ala Val Asn Phe  
 90 95 100

acc aac cct tgg gtg ctg tct gag atc gag cct ggt gcc gct gcc gtg 451  
 Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro Gly Ala Ala Ala Val  
 105 110 115

gtg ggc act ttt gag atc aag cca gag ttc ctt ctc aag gct ttg act 499  
 Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu Leu Lys Ala Leu Thr  
           120                          125                          130

ggt caa gag gga gga cca aag ggc aag ctg cca ttg act gtt cct gct 547  
 Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro Leu Thr Val Pro Ala  
           135                          140                          145

tcc atg cag gcg att gct gat tcc cct cgc gat atc cca ggc aag ttc 595  
 Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp Ile Pro Gly Lys Phe  
           150                          155                          160                          165

ctc gat gag tct tac acc tac gtg gac tcc gca ggg atg gcc tac aag 643  
 Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala Gly Met Ala Tyr Lys  
                           170                          175                          180

tac ggt cac gga ctt aat ttc tagattgtag gtagtctcgt ggg 687  
 Tyr Gly His Gly Leu Asn Phe  
                           185

&lt;210&gt; 470

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 470

Val Leu Pro Leu Asp Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val  
   1                          5                          10                          15

Thr Gly Arg Thr Lys Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala  
           20                          25                          30

Ile Arg Ala Glu Leu Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu  
           35                          40                          45

Ala Asp Leu Ala Ile Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu  
           50                          55                          60

Asp Asp Leu Glu Gly Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly  
           65                          70                          75                          80

Val Asp Val Glu Arg Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile  
                           85                          90                          95

Leu Ala Val Asn Phe Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro  
           100                          105                          110

Gly Ala Ala Ala Val Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu  
           115                          120                          125

Leu Lys Ala Leu Thr Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro  
           130                          135                          140

Leu Thr Val Pro Ala Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp  
           145                          150                          155                          160

Ile Pro Gly Lys Phe Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala  
                           165                          170                          175

Gly Met Ala Tyr Lys Tyr Gly His Gly Leu Asn Phe

185

<400> 471  
ctttaagca tttcaacatg ccaaactaat cttggacagg tatcactggc tcctcttaga 60

ttc att qqa ttt aaa gat qgc acc qqa aac atc gag cac cta gca aag 643

Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile Glu His Leu Ala Lys  
 170 175 180  
 atc acc acg cta tgc gga gat cgc ctg ttc tac ctc ggt gga ctt ccc 691  
 Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr Leu Gly Gly Leu Pro  
 185 190 195  
 acc gct gag acc ttt gca cta cca ctg ctt cag atg ggc atg agc acc 739  
 Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln Met Gly Met Ser Thr  
 200 205 210  
 tac tcc tct gca atg ttc aac ttc att cca gat ttc gca ctg agc ttc 787  
 Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp Phe Ala Leu Ser Phe  
 215 220 225  
 tac gcc gat gtt cgt gcg cag gac agc gca gca gta aag cag aag ctg 835  
 Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala Val Lys Gln Lys Leu  
 230 235 240 245  
 agc gat ttt gtg ctc ccc tac ttg gat atc cgc gat cgc gca caa ggc 883  
 Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg Asp Arg Ala Gln Gly  
 250 255 260  
 tac ggt gtc tcc att ggt aag ggc gga ctc aag gct gtt ggc cgc aac 931  
 Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys Ala Val Gly Arg Asn  
 265 270 275  
 gct ggc ggc gtt cgc cca cca ctg cgt aac ctt tcc gag caa gat atc 979  
 Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu Ser Glu Gln Asp Ile  
 280 285 290  
 gcg gac ctg tcg gat ttg ctt gcc acc tct ggc gca ggt tcc tac cgc 1027  
 Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly Ala Gly Ser Tyr Arg  
 295 300 305  
 ctt cag ttg agg tgaaagcatg atcaccgcaa ccg 1062  
 Leu Gln Leu Arg.  
 310

&lt;210&gt; 472

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 472

Met Ala Arg Phe Ser Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly  
 1 5 10 15  
 Leu Leu Ser Phe Pro Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp  
 20 25 30  
 Glu Ala Ala Tyr Val Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val  
 35 40 45  
 Ala Gly Leu Phe Ala Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr  
 50 55 60  
 Val Glu Glu Asn His Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser  
 65 70 75 80

<210> 473  
<211> 924  
<212> DNA  
<213> Corynebacterium glutamicum

```
<400> 473
gacctaaaat tcatcacctc accgttttta aggcttagaa aaatagcagt gttgggatgt 60
gaatatccat ttatgctgct gtagtcggct atgtggacgc atg gtg gca acc tct 115
Met Val Ala Thr Ser
```

	1	5	
cag ttt atc gat gac agc gag gct gcc cag gcg gta cgc gca gct att			163
Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala Val Arg Ala Ala Ile	10	15	20
gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag			211
Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu	25	30	35
cgc ggc gtt ggc gaa ggc att cgc acc gct gga gtg ccc cgc gag gag			259
Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu	40	45	50
ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga			307
Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly	55	60	65
gca gtc gcc gcg att gat gag tct ttg gcg aaa att ggc ttg gat tat			355
Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr	70	75	80
gtc gat ctg atg ctc att cac tcc cca caa cca tgg agt gat ttc cgt			403
Val Asp Leu Met Leu Ile His Ser Pro Gln Pro Trp Ser Asp Phe Arg	90	95	100
ggt ggg gac tat tca gag gga aac cgt gaa gcg tgg cgc gcg ctg gaa			451
Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala Trp Arg Ala Leu Glu	105	110	115
gat gcc tac aaa gcc gga aag att cga tcc att ggt gtc tcg aac ttc			499
Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile Gly Val Ser Asn Phe	120	125	130
ctg gag gcc gat ctg gag aat atc tta gac tcc gcg acg gtt gct cct			547
Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser Ala Thr Val Ala Pro	135	140	145
cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta			595
His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu	150	155	160
atc agt ttc tgc gat tcc aag ggc att ctg gtc gaa gca tat tca ccc			643
Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val Glu Ala Tyr Ser Pro	170	175	180
atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct			691
Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala	185	190	195
gac aag tac aac gtg agc att ccg cag cta tgc att ccg tac aca att			739
Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys Ile Arg Tyr Thr Ile	200	205	210
caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg			787
Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met	215	220	225
agc tcc aat gcg cag atc gac ttt gaa att tcc gag gaa gac atg gcg			835
Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser Glu Glu Asp Met Ala	230	235	240
			245

gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt 883  
 Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe  
                   250                  255                  260

cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac 924  
 Pro Val Tyr Ser Gly Lys  
                   265

<210> 474

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Met Val Ala Thr Ser Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala  
   1                  5                  10                  15

Val Arg Ala Ala Ile Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu  
                   20                  25                  30

Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly  
                   35                  40                  45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile  
                   50                  55                  60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys  
   65                  70                  75                  80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro  
                   85                  90                  95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala  
                   100                  105                  110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile  
                   115                  120                  125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser  
                   130                  135                  140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn  
   145                  150                  155                  160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val  
                   165                  170                  175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln  
                   180                  185                  190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys  
                   195                  200                  205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala  
                   210                  215                  220

Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser  
   225                  230                  235                  240

Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly  
 245 250 255

Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys  
 260 265

<210> 475

<211> 3561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3538)

<223> RXN00200

<400> 475

aacccggagt catttgatca gatgtggcag accaagcaag tgggaccttt cgtggtggta 60  
 acgcacaatg agtaattcct caccaaacga cccaagccct atg cgc caa gtc ggt 115  
 Met Arg Gln Val Gly  
 1 5  
 ggt aat ggg ggc cat caa cta gac tcg atc aac gtg tca gat gta gtt 163  
 Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn Val Ser Asp Val Val  
 10 15 20  
 gag tcg aag aaa cta aag ggt tct gcg caa gaa ccc ccg cag gtt gcc 211  
 Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu Pro Pro Gln Val Ala  
 25 30 35  
 ccg ggc tgg ctg aag aaa ctg gct atc tca tca ggt ctg ctt ggc ctg 259  
 Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser Gly Leu Leu Gly Leu  
 40 45 50  
 ttg atg ttt gtg ctg ttg cct ttc ctg cca gtg aac cag gtg cag tct 307  
 Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val Asn Gln Val Gln Ser  
 55 60 65  
 tcg ctg tca tgg cca caa aat ggt gag ctt tcc agc gtt aac gcc ccg 355  
 Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser Ser Val Asn Ala Pro  
 70 75 80 85  
 ctg att tcc tac gca ccg cag tcg atg gat gcg tcc atc cct gtg tcc 403  
 Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala Ser Ile Pro Val Ser  
 90 95 100  
 gcg ctg gac agt ctc aat gac aat cag tcg ttg gtg atg ggc acg ttg 451  
 Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu Val Met Gly Thr Leu  
 105 110 115  
 cct ctg gac agt acg gac gcc acc aac cgt ggt ctg ttt gtg cgc acc 499  
 Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly Leu Phe Val Arg Thr  
 120 125 130  
 atc gac ggt aac ctt gac gtg att gtt cgc ggt gag gtg ctg ttg gat 547  
 Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly Glu Val Leu Leu Asp  
 135 140 145  
 ctt tca cca aca gag gtg aac cgt ctg cca gat gat gcg atc cta gag 595



Leu 150	Ser	Pro	Thr	Glu	Val 155	Asn	Arg	Leu	Pro	Asp 160	Asp	Ala	Ile	Leu	Glu 165	
att	tcc	tcc	acc	gag	gaa	acc	acc	agc	gcg	gaa	atc	acc	ggc	acg	gca	643
Ile	Ser	Ser	Thr	Glu	Glu	Thr	Thr	Ser	Ala	Glu	Ile	Thr	Gly	Thr	Ala	
				170					175					180		
ttc	agc	ggc	gag	acc	gaa	ggc	gat	gag	cgg	cct	cag	gtc	acc	ggc	gtt	691
Phe	Ser	Gly	Glu	Thr	Glu	Gly	Asp	Glu	Arg	Pro	Gln	Val	Thr	Gly	Val	
			185					190					195			
tac	acc	gag	ctt	gtc	gac	gac	ccc	tcc	acc	gca	tcg	gcc	ctg	gcc	tca	739
Tyr	Thr	Glu	Leu	Val	Asp	Asp	Pro	Ser	Thr	Ala	Ser	Ala	Leu	Ala	Ser	
		200					205					210				
gcg	ggc	tta	aac	gtt	gat	att	gag	atc	aac	tcc	cgc	ttc	act	tca	tcc	787
Ala	Gly	Leu	Asn	Val	Asp	Ile	Glu	Ile	Asn	Ser	Arg	Phe	Thr	Ser	Ser	
	215					220					225					
ccc	agc	ctt	cta	aag	tac	gca	gcc	atc	ttc	att	ggc	ctt	gcg	tct	gtg	835
Pro	Ser	Leu	Leu	Lys	Tyr	Ala	Ala	Ile	Phe	Ile	Gly	Leu	Ala	Ser	Val	
	230				235					240					245	
ttg	gtc	tcc	ctg	tgg	aca	ctg	cac	cgc	atg	gat	att	ttg	gat	ggc	cga	883
Leu	Val	Ser	Leu	Trp	Thr	Leu	His	Arg	Met	Asp	Ile	Leu	Asp	Gly	Arg	
			250					255						260		
aaa	gca	cac	cgc	ttc	ctg	cct	gcc	aac	tgg	tac	aag	ctg	aag	cca	ctt	931
Lys	Ala	His	Arg	Phe	Leu	Pro	Ala	Asn	Trp	Tyr	Lys	Leu	Lys	Pro	Leu	
		265					270					275				
gat	ggt	gtt	gtc	gta	gcg	att	ttg	gtg	ttc	tgg	cac	ttc	ctt	ggc	gcc	979
Asp	Gly	Val	Val	Val	Ala	Ile	Leu	Val	Phe	Trp	His	Phe	Leu	Gly	Ala	
	280					285						290				
aac	acc	tct	gac	gac	ggc	ttc	atc	atg	acc	atg	gcc	cgc	gtg	tcc	cag	1027
Asn	Thr	Ser	Asp	Asp	Gly	Phe	Ile	Met	Thr	Met	Ala	Arg	Val	Ser	Gln	
	295					300					305					
aac	gcg	gat	tat	atg	gcc	aac	tac	tac	cgc	tgg	ttc	ggt	gtc	cca	gaa	1075
Asn	Ala	Asp	Tyr	Met	Ala	Asn	Tyr	Tyr	Arg	Trp	Phe	Gly	Val	Pro	Glu	
	310				315					320					325	
tca	cca	ttc	ggc	gca	cca	tat	tac	gac	ttg	ctg	gct	ctg	atg	gcc	tac	1123
Ser	Pro	Phe	Gly	Ala	Pro	Tyr	Tyr	Asp	Leu	Leu	Ala	Leu	Met	Ala	Tyr	
			330						335					340		
atc	tca	acc	tca	tca	atc	tgg	ctt	cgt	cta	ccc	gca	ttg	ctc	gct	gga	1171
Ile	Ser	Thr	Ser	Ser	Ile	Trp	Leu	Arg	Leu	Pro	Ala	Leu	Leu	Ala	Gly	
			345					350					355			
ctg	atc	atg	tgg	ttc	gtg	atc	acc	aga	gag	gtc	atg	cca	cgg	ttt	ggc	1219
Leu	Ile	Met	Trp	Phe	Val	Ile	Thr	Arg	Glu	Val	Met	Pro	Arg	Phe	Gly	
		360				365						370				
tca	ttg	gtt	aac	ggt	cgc	cgc	gtt	gcg	cac	tgg	tct	gca	gcc	atg	gtg	1267
Ser	Leu	Val	Asn	Gly	Arg	Arg	Val	Ala	His	Trp	Ser	Ala	Ala	Met	Val	
	375					380					385					
ttc	ctg	gcg	ttc	tgg	ctt	cca	tac	aac	aac	ggc	act	cgc	cca	gag	cca	1315
Phe	Leu	Ala	Phe	Trp	Leu	Pro	Tyr	Asn	Asn	Gly	Thr	Arg	Pro	Glu	Pro	

390	395	400	405	
atc atc gcg atg gga gct cta ctt gcg tgg gtt tcc ttc gag cgc gct				1363
Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val Ser Phe Glu Arg Ala	410	415	420	
atc gct acc tcc agg ttg ttg ccc gct gcc att ggt gtc att atc gcc				1411
Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile Gly Val Ile Ile Ala	425	430	435	
acc att tcc ctg gca tca ggc ccc acc ggt cta atg gca gtt gct gcg				1459
Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu Met Ala Val Ala Ala	440	445	450	
ttg ctg gtc agt ttg tcc gcg ttg att cgc att ctt tat agg cgc ttg				1507
Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile Leu Tyr Arg Arg Leu	455	460	465	
ccg ctt att ggg gcg tcg agg ggg gcg tcg aaa agc aaa gtc ttt ggc				1555
Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys Ser Lys Val Phe Gly	470	475	480	485
gct tcg atg gct atg ctt gcc cca ttc ctt gcg tct ggc acc gcg att				1603
Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala Ser Gly Thr Ala Ile	490	495	500	
ctc atc gcc gtt ttt ggc gat cag act ctg tca acc gtc atg gaa tcc				1651
Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser Thr Val Met Glu Ser	505	510	515	
atc agc gtg cgc tcc gcg aag ggc ccg gca ctg acc tgg tac cac gaa				1699
Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu Thr Trp Tyr His Glu	520	525	530	
tat gtg cgc tac caa acc gtc atg gaa caa acc gtt gat ggt tcc ttc				1747
Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr Val Asp Gly Ser Phe	535	540	545	
acc cgc cgt ttt gct gtg ctg atg ctc atg gcg tgt ctg gct att gtg				1795
Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala Cys Leu Ala Ile Val	550	555	560	565
gtc atc gcg atc ctg cgt tac ggc cgc att cca ggc gct gcg aag gga				1843
Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro Gly Ala Ala Lys Gly	570	575	580	
cca tca ctg cgt ttg atg atg gtc att ttc ggc acc atg ttc ttc atg				1891
Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly Thr Met Phe Phe Met	585	590	595	
atg ttc acc cca acc aag tgg act cac cac ttc ggt gtc tac gca gga				1939
Met Phe Thr Pro Thr Lys Trp Thr His His Phe Gly Val Tyr Ala Gly	600	605	610	
ctt gcc ggc gca ttg gcc gga ctt gct gcc gtg ggg ctg tcc tat gtt				1987
Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val Gly Leu Ser Tyr Val	615	620	625	
gcg gtg aaa tca cca cgc atg cgc acc att tcc atc ggt gcg ttc ctc				2035
Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser Ile Gly Ala Phe Leu	630	635	640	645

ttc ctg ctg gcg ctg gct ctc gca ggc gtg aac gga ttc tgg tac acc	2083
Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn Gly Phe Trp Tyr Thr	
650 655 660	
tcc agc tac gcc gtg cca tgg tgg gat aaa acc atc cag atc aag ggc	2131
Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr Ile Gln Ile Lys Gly	
665 670 675	
atc gaa gca tcc acc gta gtg ctc gtg atc gcc gtg atc gtg ctg atc	2179
Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala Val Ile Val Leu Ile	
680 685 690	
atc ggt gtt att caa tcc ttt gtc cac gat gtg aaa acc gcg caa gcc	2227
Ile Gly Val Ile Gln Ser Phe Val His Asp Val Lys Thr Ala Gln Ala	
695 700 705	
gaa acc aat cac tcc atg ggc gaa ctc gtg gcg gaa gat gaa gca aag	2275
Glu Thr Asn His Ser Met Gly Glu Leu Val Ala Glu Asp Glu Ala Lys	
710 715 720 725	
cgc gag cgt gcc tcc agg ttc acc ggc ctt gcg gcc tcc cct atc gca	2323
Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala Ala Ser Pro Ile Ala	
730 735 740	
gga gtg tcc gcc ctc gtt gtg ctg att acc tgc gca tcc atg ggc aaa	2371
Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys Ala Ser Met Gly Lys	
745 750 755	
ggc ttt gtg gac caa tac ccc gcg tac tcc gtg ggt ctt ggc aac ctc	2419
Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val Gly Leu Gly Asn Leu	
760 765 770	
cgc tcc ctg acc ggc aac aca tgt ggc ctt gcc tcc gac gcc atg ctg	2467
Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala Ser Asp Ala Met Leu	
775 780 785	
gaa acc aac tcc aac gat tcc ttc ctc act cca gtg aac tcc aca ctt	2515
Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro Val Asn Ser Thr Leu	
790 795 800 805	
ggc gag tcc ctg gaa tcc gaa gat att cgc ggc ttt agt gct gcc ggc	2563
Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly Phe Ser Ala Ala Gly	
810 815 820	
atc cca cca tca atc agc cag gac caa gca gac ctg tct gct gtt ggt	2611
Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp Leu Ser Ala Val Gly	
825 830 835	
gcc att gcc aac act gac gac tcc acc gaa acc ggc gga tcc gac gaa	2659
Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr Gly Gly Ser Asp Glu	
840 845 850	
tca tcc gga caa tcc acc ggc aac acc ggc ggt gtc cga ggc tcc gaa	2707
Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly Val Arg Gly Ser Glu	
855 860 865	
ggc atc aac ggc tcc aac gcc cgc ctg cca ttc aac ctg gac tac acc	2755
Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe Asn Leu Asp Tyr Thr	
870 875 880 885	

caa gtt cca gtc gtc ggc tcc tgg tcc gct ggc acc caa aac cca gca	2803
Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly Thr Gln Asn Pro Ala	
890 895 900	
aac atc acc acc gac tgg tac gaa atc cca gaa gcc acc gaa gaa gca	2851
Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu Ala Thr Glu Glu Ala	
905 910 915	
ccc atc atc gtg gta tct gca gca ggt cgc atc gaa cac tac gac atc	2899
Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile Glu His Tyr Asp Ile	
920 925 930	
aac ggc gtc cgc caa tcc gga caa tcc gtc atg ctc gaa tac ggt cgc	2947
Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met Leu Glu Tyr Gly Arg	
935 940 945	
ctt cgc gat aac ggc gac gtt gaa gac ctc ggc gaa gcc atg atg tac	2995
Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly Glu Ala Met Met Tyr	
950 955 960 965	
gac atc ggc ccc gag cca tcc tgg cgc aac ctc cgc tac cca ctt gac	3043
Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu Arg Tyr Pro Leu Asp	
970 975 980	
caa ctc cca gaa gaa gcg gac gtc gtg cgc atc gtc gcc acc gac gtc	3091
Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile Val Ala Thr Asp Val	
985 990 995	
aac ctc gac gaa gac caa tgg gta gca ctg acg cca cca cgc gta cct	3139
Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr Pro Pro Arg Val Pro	
1000 1005 1010	
aac cta gat tct ctg aac aac gtc atc gga tcc gaa acc cca gga ctc	3187
Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser Glu Thr Pro Gly Leu	
1015 1020 1025	
ctc gac tgg gca gtt ggc ctg caa ttc cca tgc caa cgc acc ttc gac	3235
Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys Gln Arg Thr Phe Asp	
1030 1035 1040 1045	
cac tac gcc gga gtc acc gag att cct gaa tac cga atc tcc cca gac	3283
His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp	
1050 1055 1060	
cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc	3331
His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly	
1065 1070 1075	
gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg	3379
Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro	
1080 1085 1090	
tcc tac ctc cgc aac gac tgg ggc cgc gac tgg ggt tcc atc gaa cgc	3427
Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg	
1095 1100 1105	
tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac	3475
Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp	
1110 1115 1120 1125	
atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat	3523

Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His  
 1130 1135 1140

atg aag gta gat gaa taagaccttc agtactggaa gtt 3561  
 Met Lys Val Asp Glu  
 1145

<210> 476  
 <211> 1146  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 476  
 Met Arg Gln Val Gly Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn  
 1 5 10 15

Val Ser Asp Val Val Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu  
 20 25 30

Pro Pro Gln Val Ala Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser  
 35 40 45

Gly Leu Leu Gly Leu Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val  
 50 55 60

Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser  
 65 70 75 80

Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala  
 85 90 95

Ser Ile Pro Val Ser Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu  
 100 105 110

Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly  
 115 120 125

Leu Phe Val Arg Thr Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly  
 130 135 140

Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp  
 145 150 155 160

Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu  
 165 170 175

Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro  
 180 185 190

Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala  
 195 200 205

Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser  
 210 215 220

Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile  
 225 230 235 240

Gly Leu Ala Ser Val Leu Val Ser Leu Trp Thr Leu His Arg Met Asp  
 245 250 255

Ile Leu Asp Gly Arg Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr  
 260 265 270  
 Lys Leu Lys Pro Leu Asp Gly Val Val Val Ala Ile Leu Val Phe Trp  
 275 280 285  
 His Phe Leu Gly Ala Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met  
 290 295 300  
 Ala Arg Val Ser Gln Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp  
 305 310 315 320  
 Phe Gly Val Pro Glu Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu  
 325 330 335  
 Ala Leu Met Ala Tyr Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro  
 340 345 350  
 Ala Leu Leu Ala Gly Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val  
 355 360 365  
 Met Pro Arg Phe Gly Ser Leu Val Asn Gly Arg Arg Val Ala His Trp  
 370 375 380  
 Ser Ala Ala Met Val Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly  
 385 390 395 400  
 Thr Arg Pro Glu Pro Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val  
 405 410 415  
 Ser Phe Glu Arg Ala Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile  
 420 425 430  
 Gly Val Ile Ile Ala Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu  
 435 440 445  
 Met Ala Val Ala Ala Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile  
 450 455 460  
 Leu Tyr Arg Arg Leu Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys  
 465 470 475 480  
 Ser Lys Val Phe Gly Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala  
 485 490 495  
 Ser Gly Thr Ala Ile Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser  
 500 505 510  
 Thr Val Met Glu Ser Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu  
 515 520 525  
 Thr Trp Tyr His Glu Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr  
 530 535 540  
 Val Asp Gly Ser Phe Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala  
 545 550 555 560  
 Cys Leu Ala Ile Val Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro  
 565 570 575

Gly Ala Ala Lys Gly Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly  
 580 585 590  
 Thr Met Phe Phe Met Met Phe Thr Pro Thr Lys Trp Thr His His Phe  
 595 600 605  
 Gly Val Tyr Ala Gly Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val  
 610 615 620  
 Gly Leu Ser Tyr Val Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser  
 625 630 635 640  
 Ile Gly Ala Phe Leu Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn  
 645 650 655  
 Gly Phe Trp Tyr Thr Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr  
 660 665 670  
 Ile Gln Ile Lys Gly Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala  
 675 680 685  
 Val Ile Val Leu Ile Ile Gly Val Ile Gln Ser Phe Val His Asp Val  
 690 695 700  
 Lys Thr Ala Gln Ala Glu Thr Asn His Ser Met Gly Glu Leu Val Ala  
 705 710 715 720  
 Glu Asp Glu Ala Lys Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala  
 725 730 735  
 Ala Ser Pro Ile Ala Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys  
 740 745 750  
 Ala Ser Met Gly Lys Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val  
 755 760 765  
 Gly Leu Gly Asn Leu Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala  
 770 775 780  
 Ser Asp Ala Met Leu Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro  
 785 790 795 800  
 Val Asn Ser Thr Leu Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly  
 805 810 815  
 Phe Ser Ala Ala Gly Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp  
 820 825 830  
 Leu Ser Ala Val Gly Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr  
 835 840 845  
 Gly Gly Ser Asp Glu Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly  
 850 855 860  
 Val Arg Gly Ser Glu Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe  
 865 870 875 880  
 Asn Leu Asp Tyr Thr Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly  
 885 890 895  
 Thr Gln Asn Pro Ala Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu

900	905	910
Ala Thr Glu Glu Ala Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile 915 920 925		
Glu His Tyr Asp Ile Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met 930 935 940		
Leu Glu Tyr Gly Arg Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly 945 950 955 960		
Glu Ala Met Met Tyr Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu 965 970 975		
Arg Tyr Pro Leu Asp Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile 980 985 990		
Val Ala Thr Asp Val Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr 995 1000 1005		
Pro Pro Arg Val Pro Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser 1010 1015 1020		
Glu Thr Pro Gly Leu Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys 1025 1030 1035 1040		
Gln Arg Thr Phe Asp His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr 1045 1050 1055		
Arg Ile Ser Pro Asp His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln 1060 1065 1070		
Asp Trp Ala Gly Gly Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn 1075 1080 1085		
Ala Tyr Glu Ile Pro Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp 1090 1095 1100		
Gly Ser Ile Glu Arg Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala 1105 1110 1115 1120		
Pro Lys Val Ala Asp Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu 1125 1130 1135		
Trp Asn Pro Gly His Met Lys Val Asp Glu 1140 1145		

&lt;210&gt; 477

&lt;211&gt; 1509

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1486)

&lt;223&gt; RXN01175

&lt;400&gt; 477

tcgcgtctct tagtcgatct gctcccatc cataggttg gagaaaactt aactgttatt 60



ccatttcctta aaacaccgat atcgtgctat gaataggggt gtg agt tgg aca gtt 115  
Val Ser Trp Thr Val 5

gat atc cct aaa gaa gtt ctc cct gat ttg cca cca ttg cca gaa ggc 163  
Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro Pro Leu Pro Glu Gly 20

atg cag cag cag ttc gag gac acc att tcc cgt gac gct aag cag caa 211  
Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg Asp Ala Lys Gln Gln 35

cct acg tgg gat cgt gca cag gca gaa aac gtg cgc aag atc ctt gag 259  
Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val Arg Lys Ile Leu Glu 50

tcg gtt cct cca atc gtt gtt gcc cct gag gta ctt gag ctg aag cag 307  
Ser Val Pro Pro Ile Val Val Ala Pro Glu Val Leu Glu Leu Lys Gln 65

aag ctt gct gat gtt gcc aac ggt aag gcc ttc ctc ttg cag ggt ggt 355  
Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe Leu Leu Gln Gly Gly 85

gac tgt gcg gaa act ttc gag tca aac act gag ccg cac att cgc gcc 403  
Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu Pro His Ile Arg Ala 100

aac gta aag act ctg ctg cag atg gca gtt gtt ttg acc tac ggt gca 451  
Asn Val Lys Thr Leu Leu Gln Met Ala Val Val Leu Thr Tyr Gly Ala 115

tcc act cct gtg atc aag atg gct cgt att gct ggt cag tac gca aag 499  
Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala Gly Gln Tyr Ala Lys 130

cct cgc tct tct gat ctg gat gga aat ggt ctg cca aac tac cgt ggc 547  
Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu Pro Asn Tyr Arg Gly 145

gat atc gtc aac ggt gtg gag gca acc cca gag gct cgt cgc cac gat 595  
Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu Ala Arg Arg His Asp 165

cct gcc cgc atg atc cgt gct tac gct aac gct tct gct gcg atg aac 643  
Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala Ser Ala Ala Met Asn 180

ttg gtg cgc gcg ctc acc agc tct ggc acc gct gat ctt tac cgt ctc 691  
Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala Asp Leu Tyr Arg Leu 195

agc gag tgg aac cgc gag ttc gtt gcg aac tcc cca gct ggt gca cgc 739  
Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser Pro Ala Gly Ala Arg 210

tac gag gct ctt gct cgt gag atc gac tcc ggt ctg cgc ttc atg gaa 787  
Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly Leu Arg Phe Met Glu 225

gca tgt ggc gtg tcc gat gag tcc ctg cgt gct gca gat atc tac tgc 835

Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala Ala Asp Ile Tyr Cys	
230 235 240 245	
tcc cac gag gct ttg ctg gtg gat tac gag cgt tcc atg ctg cgt ctt	883
Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg Ser Met Leu Arg Leu	
250 255 260	
gca acc gat gag gaa ggc aac gag gaa ctt tac gat ctt tca gct cac	931
Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr Asp Leu Ser Ala His	
265 270 275	
cag ctg tgg atc ggc gag cgc acc cgt ggc atg gat gat ttc cat gtg	979
Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met Asp Asp Phe His Val	
280 285 290	
aac ttc gca tcc atg atc tct aac cca atc ggc atc aag att ggt cct	1027
Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly Ile Lys Ile Gly Pro	
295 300 305	
ggt atc acc cct gaa gag gct gtt gca tac gct gac aag ctc gat ccg	1075
Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala Asp Lys Leu Asp Pro	
310 315 320 325	
aac ttc gag cct ggc cgt ttg acc atc gtt gct cgc atg ggc cac gac	1123
Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala Arg Met Gly His Asp	
330 335 340	
aag gtt cgc tcc gta ctt cct ggt gtt atc cag gct gtt gag gca tcc	1171
Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln Ala Val Glu Ala Ser	
345 350 355	
gga cac aag gtt att tgg cag tcc gat ccg atg cac ggc aac act ttc	1219
Gly His Lys Val Ile Trp Gln Ser Asp Pro Met His Gly Asn Thr Phe	
360 365 370	
acc gca tcc aat ggc tac aag acc cgt cac ttc gac aag gtt atc gat	1267
Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe Asp Lys Val Ile Asp	
375 380 385	
gag gtc cag ggc ttc ttc gag gtc cac cgc gca ttg ggc acc cac cca	1315
Glu Val Gln Gly Phe Phe Glu Val His Arg Ala Leu Gly Thr His Pro	
390 395 400 405	
ggc gga atc cac att gag ttc act ggt gaa gat gtc acc gag tgc ctc	1363
Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp Val Thr Glu Cys Leu	
410 415 420	
ggt ggc gct gaa gac atc acc gat gtt gat ctg cca ggc cgc tac gag	1411
Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu Pro Gly Arg Tyr Glu	
425 430 435	
tcc gca tgc gat cct cgc ctg aac act cag cag tct ttg gag ttg gct	1459
Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln Ser Leu Glu Leu Ala	
440 445 450	
ttc ctc gtt gca gaa atg ctg cgt aac taagctttta gaccaactct	1506
Phe Leu Val Ala Glu Met Leu Arg Asn	
455 460	
aaa	1509

&lt;210&gt; 478

&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 478

Val Ser Trp Thr Val Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro  
 1 5 10 15

Pro Leu Pro Glu Gly Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg  
 20 25 30

Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val  
 35 40 45

Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val  
 50 55 60

Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe  
 65 70 75 80

Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu  
 85 90 95

Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val  
 100 105 110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala  
 115 120 125

Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu  
 130 135 140

Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu  
 145 150 155 160

Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala  
 165 170 175

Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala  
 180 185 190

Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser  
 195 200 205

Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly  
 210 215 220

Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala  
 225 230 235 240

Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg  
 245 250 255

Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr  
 260 265 270

Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met  
 275 280 285

Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly  
 290 295 300  
 Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala  
 305 310 315 320  
 Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala  
 325 330 335  
 Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln  
 340 345 350  
 Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met  
 355 360 365  
 His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe  
 370 375 380  
 Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala  
 385 390 395 400  
 Leu Gly Thr His Pro Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp  
 405 410 415  
 Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu  
 420 425 430  
 Pro Gly Arg Tyr Glu Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln  
 435 440 445  
 Ser Leu Glu Leu Ala Phe Leu Val Ala Glu Met Leu Arg Asn  
 450 455 460

&lt;210&gt; 479

&lt;211&gt; 984

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(961)

&lt;223&gt; RXN01376

&lt;400&gt; 479

tcctcatcgg ttatcgggag tggcggatac ttcttgcaaa cttaaaccac tatgctttcg 60

cttcgtgagt actttgaaat ccccatcgc tgtgatcaca gtg acc tat tca cca 115  
 Val Thr Tyr Ser Pro  
 1 5

ggt aaa tac ttg gcg tcg ttc ctg gat tct ttg cct ggt gcg act tca 163  
 Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser  
 10 15 20

cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt 211  
 Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val  
 25 30 35

cct gag cag gca gca gcc tca cgc agc aac gtg gag ttc ctc tca act 259  
 Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr

40	45	50	
ggc ggc aac tta ggc tac gga acg gct att aat att gcc gcc cga tcg Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn Ile Ala Ala Arg Ser 55 60 65			307
ttg cgt gcg cgc cgg gag gca gga gag atc gat ggg gag ttc ttc ctc Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp Gly Glu Phe Phe Leu 70 75 80 85			355
gtc tca aac cct gat gtt gtt ttt gac gaa gac tct att gat caa ttg Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu 90 95 100			403
ctt gaa tgt gcg aaa cgt cac cct gaa gca gga gcg gtt ggc ccg ttg Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu 105 110 115			451
atc cgt gag gcg gac ggt tcg gcg tat ccg tcg gct ccg gcg gta ccc Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro 120 125 130			499
act ttg gcg aat ggc att ggt cac gct ttg ttg ggt gct gtg tgg aaa Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu Gly Ala Val Trp Lys 135 140 145			547
tcc aat ccg tgg tcg gcg gct tac cgt gac gat gaa gat atg gac act Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr 150 155 160 165			595
gag cgc act gct ggc tgg ctg tcg gga tcg tgc ctg tta tta agg tgg Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Leu Arg Trp 170 175 180			643
gat gcg ttt gat cga gtt ggt ggt ttt gat gag cgc tac ttc atg tac Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr 185 190 195			691
atg gaa gac gtt gac ctg gga gat ccg ctg gtt cgc gcc ggt ttc acc Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr 200 205 210			739
aac gtc ttt tgc cca agt gcg cag atc atc cac gcg aaa ggt cat gtt Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His Ala Lys Gly His Val 215 220 225			787
gcg ggt aaa aac cca gag aac atg ttg ccc gca cac cac gag agc gcg Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala His His Glu Ser Ala 230 235 240 245			835
tat cgc ttc cag gct gat cgc ctc gcg aag ccg tgg caa gcc cca att Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro Trp Gln Ala Pro Ile 250 255 260			883
cgg ttg gct ctg cga att ggt ttg aaa tta cga gcc gga gtc gcg gtt Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg Ala Gly Val Ala Val 265 270 275			931
ggt gtc tct aag atg aga acg aaa gcc tct tagaccgtcg acgaccaccg Gly Val Ser Lys Met Arg Thr Lys Ala Ser 280 285			981

gac

984

&lt;210&gt; 480

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 480

Val Thr Tyr Ser Pro Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu  
 1 5 10 15  
 Pro Gly Ala Thr Ser Arg Asp Thr His Val Val Met Ala Asp Asn Gly  
 20 25 30  
 Ser Val Asp Gly Val Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val  
 35 40 45  
 Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn  
 50 55 60  
 Ile Ala Ala Arg Ser Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp  
 65 70 75 80  
 Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp  
 85 90 95  
 Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly  
 100 105 110  
 Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser  
 115 120 125  
 Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu  
 130 135 140  
 Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp  
 145 150 155 160  
 Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys  
 165 170 175  
 Leu Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu  
 180 185 190  
 Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val  
 195 200 205  
 Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His  
 210 215 220  
 Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala  
 225 230 235 240  
 His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro  
 245 250 255  
 Trp Gln Ala Pro Ile Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg  
 260 265 270

Ala Gly Val Ala Val Gly Val Ser Lys Met Arg Thr Lys Ala Ser  
 275 280 285

<210> 481  
 <211> 1002  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(979)  
 <223> RXN01631

<400> 481  
 gccagttgag gatgctctca cagtcgctcg cattgtcagt gcatgctacg aatccgacaa 60

caaccagggc atttccgtaa acatctaaga ggagcactcc atg aaa cca caa ctt 115  
 Met Lys Pro Gln Leu  
 1 5

att gca tct tgc tgg acc agc gcg gga gac gcc gca ccc gat cgt gac 163  
 Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala Ala Pro Asp Arg Asp  
 10 15 20

gat ctc agc agc cca gta gca atc gat gag cgc atc gct cta gtc gct 211  
 Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala  
 25 30 35

gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa 259  
 Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys  
 40 45 50

gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct 307  
 Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala  
 55 60 65

gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg 355  
 Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala  
 70 75 80 85

act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt 403  
 Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe  
 90 95 100

gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga 451  
 Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly  
 105 110 115

gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt 499  
 Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe  
 120 125 130

act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg 547  
 Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu  
 135 140 145

gaa gca act ccg ttt tct cac ctg aag acc atc tac gac gcg ctg gaa 595  
 Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile Tyr Asp Ala Leu Glu  
 150 155 160 165

gtt gtc agc cat tcc gat agc cca tcg gct gga ctc atg gtt gat atc 643  
 Val Val Ser His Ser Asp Ser Pro Ser Ala Gly Leu Met Val Asp Ile  
 170 175 180  
 tgg cac acc gcg aaa atc gga atc ccc aac gat gaa ctg tgg cgc aac 691  
 Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp Glu Leu Trp Arg Asn  
 185 190 195  
 att cca ctg tcc aag gtc aac gca gtg gag gtt gat gat ggt ttc att 739  
 Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val Asp Asp Gly Phe Ile  
 200 205 210  
 gac acc cca att gat ctt ttc gat gac tcc acc aac cgt cgc gcg tac 787  
 Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr Asn Arg Arg Ala Tyr  
 215 220 225  
 tgc ggt gaa gcc gaa ttt gat ccc gca agc ttc atc cgt gcc gcc atc 835  
 Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe Ile Arg Gly Ala Ile  
 230 235 240 245  
 gac gcc ggt tgg acg gcc gca tat ggt gtg gaa att att tcc gca gag 883  
 Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu Ile Ile Ser Ala Glu  
 250 255 260  
 cac cga agc ctc ccg gtg aaa gaa ggg ctg caa cgt gct ttc gac acc 931  
 His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln Arg Ala Phe Asp Thr  
 265 270 275  
 acc atc gca gcg ttt gaa caa gct gct cgt ctc gcc ccc tcc act aac 979  
 Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu Ala Pro Ser Thr Asn  
 280 285 290  
 tgatctttga aaggctgaaa aaa 1002

&lt;210&gt; 482

&lt;211&gt; 293

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 482

Met Lys Pro Gln Leu Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala  
 1 5 10 15  
 Ala Pro Asp Arg Asp Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg  
 20 25 30  
 Ile Ala Leu Val Ala Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His  
 35 40 45  
 Ala Asp Leu Ile Lys Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg  
 50 55 60  
 Arg Arg Ile His Ala Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu  
 65 70 75 80  
 Asn Gly Trp Trp Ala Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val  
 85 90 95  
 Arg Ala Asp Leu Phe Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile  
 100 105 110



Lys Val Gly Ala Gly Glu Gly Thr Asn Gly Val Val Pro Ile Ala His  
115 120 125

Met Ala Ser Ala Phe Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly  
130 135 140

Val Lys Leu Ala Leu Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile  
145 150 155 160

Tyr Asp Ala Leu Glu Val Val Ser His Ser Asp Ser Pro Ser Ala Gly  
165 170 175

Leu Met Val Asp Ile Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp  
180 185 190

Glu Leu Trp Arg Asn Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val  
195 200 205

Asp Asp Gly Phe Ile Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr  
210 215 220

Asn Arg Arg Ala Tyr Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe  
225 230 235 240

Ile Arg Gly Ala Ile Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu  
245 250 255

Ile Ile Ser Ala Glu His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln  
260 265 270

Arg Ala Phe Asp Thr Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu  
275 280 285

Ala Pro Ser Thr Asn  
290

<210> 483

<211> 990

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXN01593

<400> 483

atatgacagc cttcttcttg atctagatgg aaccgtctac gagggcggcc gagccattga 60

gcacgtagtt tctgcgctct ctggcgccgg cctaccgctc atg tat gtc acc aat 115  
Met Tyr Val Thr Asn  
1 5

aat gcc tcc cgt gct ccg gag gtg gtg gct gcg caa ctc cgt gag att 163  
Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala Gln Leu Arg Glu Ile  
10 15 20

ggc ctt gcc gac acc act gcg gac aat gtg atg aca tct gct caa gct 211  
Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met Thr Ser Ala Gln Ala

25	30	35	
gcc tgc aag atg gcg gcg gag aag att ccc gct gga tcc aag gtg tat Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala Gly Ser Lys Val Tyr 40 45 50			259
gtt ttg ggt tca gaa tcc ttc cgc gag cta gct act gaa gct ggt ttt Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala Thr Glu Ala Gly Phe 55 60 65			307
gtg gtg gtt gat tgc gct gat gat aaa cct gtg gct gtg ctt cac ggc Val Val Val Asp Ser Ala Asp Asp Lys Pro Val Ala Val Leu His Gly 70 75 80 85			355
cac aac cct gag acc ggt tgg gct cag ttg agc gag gct gcg ctg tca His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser Glu Ala Ala Leu Ser 90 95 100			403
att aat gct ggc gcg cag tat ttt gca tca aat ttg gat tcc acc ctt Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn Leu Asp Ser Thr Leu 105 110 115			451
ccc atg gaa cgc ggt cgt cac att ggc aac ggt tcc atg gtg gct gcc Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly Ser Met Val Ala Ala 120 125 130			499
gtg gtc aac gcg act ggc gta aag cct ctt tcc gca ggt aag cca ggc Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser Ala Gly Lys Pro Gly 135 140 145			547
ccc gcg atg ttc tat gcg ggg gct gaa act ctt aat tct tca aag cct Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu Asn Ser Ser Lys Pro 150 155 160 165			595
ttg gct gtc ggc gat cgt ctc gat acc gat atc gcc ggc gga aac gct Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile Ala Gly Gly Asn Ala 170 175 180			643
gca ggc atg gac aca ttc cag gtc ctg acc ggc gtc agc ggc tac tac Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly Val Ser Gly Tyr Tyr 185 190 195			691
gat ttg gtg cgc gcc att ccc aga gca gcg ccc cac cta tat cgc cac Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro His Leu Tyr Arg His 200 205 210			739
ctc gat gca gga tct cta cag cga tcc ggg cga gct caa gcc agg tgc Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg Ala Gln Ala Arg Cys 215 220 225			787
cca ggg cgg ttt ttc agc gct tat cga cgg cga cac cct ggt cat ttc Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg His Pro Gly His Phe 230 235 240 245			835
cgg cgg cga tgc cgg cgc aac tcc ggt tgc agc act ccg cac tgc gtt Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser Thr Pro His Cys Val 250 255 260			883
gga tgt ggc ctg ggc ggc cac aga gca gtc acc gag gta cgc gct gat Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr Glu Val Arg Ala Asp 265 270 275			931

tca gag gta gct gct act gca ttg cag agc tgg tgg taaacggtga 977  
 Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp Trp  
           280                          285

attcaccaaa gcc 990

<210> 484

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

Met Tyr Val Thr Asn Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala  
   1                          5                          10                          15

Gln Leu Arg Glu Ile Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met  
           20                          25                          30

Thr Ser Ala Gln Ala Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala  
           35                          40                          45

Gly Ser Lys Val Tyr Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala  
           50                          55                          60

Thr Glu Ala Gly Phe Val Val Val Asp Ser Ala Asp Asp Lys Pro Val  
           65                          70                          75                          80

Ala Val Leu His Gly His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser  
                           85                          90                          95

Glu Ala Ala Leu Ser Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn  
           100                          105                          110

Leu Asp Ser Thr Leu Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly  
           115                          120                          125

Ser Met Val Ala Ala Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser  
           130                          135                          140

Ala Gly Lys Pro Gly Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu  
           145                          150                          155                          160

Asn Ser Ser Lys Pro Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile  
                           165                          170                          175

Ala Gly Gly Asn Ala Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly  
           180                          185                          190

Val Ser Gly Tyr Tyr Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro  
           195                          200                          205

His Leu Tyr Arg His Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg  
           210                          215                          220

Ala Gln Ala Arg Cys Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg  
           225                          230                          235                          240

His Pro Gly His Phe Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser  
                           245                          250                          255

Thr Pro His Cys Val Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr  
 260 265 270

Glu Val Arg Ala Asp Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp  
 275 280 285

Trp

<210> 485

<211> 1173

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1150)

<223> RXN00337

<400> 485

ggacgcttat tggtagcat tcggattacg ccggtggtgt ggtgctggcg gctaatagcga 60  
 attgccggac tgcggctgcc gtcaataaag aaccgcgacg atg ttg tta acg tat 115  
 Met Leu Leu Thr Tyr  
 1 5  
 gcg ttt gtg gat gtg gag gga ggc gtc gaa aag cat tct tta agc act 163  
 Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr  
 10 15 20  
 gcg gac att gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt 211  
 Ala Asp Ile Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val  
 25 30 35  
 ttg ggg cgg cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc 259  
 Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala  
 40 45 50  
 cgg ttg ggc ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg 307  
 Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser  
 55 60 65  
 cgt gac aca aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag 355  
 Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu  
 70 75 80 85  
 ggg gtg ggg ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg 403  
 Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu  
 90 95 100  
 gcg ctg tat cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att 451  
 Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile  
 105 110 115  
 gcg gag att tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg 499  
 Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val  
 120 125 130  
 ttg cgt gcg cgg cac acc gtg gcg ttg cgg ggt gaa act gga cag att 547

Leu	Arg	Ala	Arg	His	Thr	Val	Ala	Leu	Arg	Gly	Glu	Thr	Gly	Gln	Ile		
135						140					145						
tcg	gtg	gtt	gat	tac	gcc	gat	ggg	tcg	gtc	act	cag	gcg	cca	cat	ccg	595	
Ser	Val	Val	Asp	Tyr	Ala	Asp	Gly	Ser	Val	Thr	Gln	Ala	Pro	His	Pro		
150					155					160					165		
gtg	agt	cgt	tcc	gct	ggg	ttg	tcg	gca	ttt	gtt	gtt	gct	gcg	caa	act	643	
Val	Ser	Arg	Ser	Ala	Gly	Leu	Ser	Ala	Phe	Val	Val	Ala	Ala	Gln	Thr		
				170					175					180			
gaa	act	gat	ccg	agc	att	tac	cgc	gag	atc	tat	gct	cga	cat	gcg	ttt	691	
Glu	Thr	Asp	Pro	Ser	Ile	Tyr	Arg	Glu	Ile	Tyr	Ala	Arg	His	Ala	Phe		
			185					190					195				
atc	gat	gaa	gct	gcg	cgc	gct	ttc	agt	gtg	gaa	tct	ttg	cgg	ttg	ctt	739	
Ile	Asp	Glu	Ala	Ala	Arg	Ala	Phe	Ser	Val	Glu	Ser	Leu	Arg	Leu	Leu		
		200				205						210					
ccc	gac	gct	tcc	act	cgt	gtt	gtg	gat	tgg	ttg	cag	gcc	gtg	att	gag	787	
Pro	Asp	Ala	Ser	Thr	Arg	Val	Val	Asp	Trp	Leu	Gln	Ala	Val	Ile	Glu		
		215				220					225						
gtg	act	ggg	cga	gag	gat	ctg	ccc	tcg	att	gaa	caa	gcc	cag	cgc	tgg	835	
Val	Thr	Gly	Arg	Glu	Asp	Leu	Pro	Ser	Ile	Glu	Gln	Ala	Gln	Arg	Trp		
230					235					240					245		
ttg	aat	ctg	tgg	gaa	aac	gaa	acc	cgg	cgc	gct	cag	agg	aca	gcc	aat	883	
Leu	Asn	Leu	Trp	Glu	Asn	Glu	Thr	Arg	Arg	Ala	Gln	Arg	Thr	Ala	Asn		
				250				255						260			
gcc	ctg	cgt	tcg	aga	agg	ctg	agt	gag	ttt	tct	gag	ctg	ctg	atg	gaa	931	
Ala	Leu	Arg	Ser	Arg	Arg	Leu	Ser	Glu	Phe	Ser	Glu	Leu	Leu	Met	Glu		
			265					270					275				
tcc	caa	gat	gat	ttg	agc	gac	acc	ttc	gat	ttc	ccc	cct	gct	gat	ttg	979	
Ser	Gln	Asp	Asp	Leu	Ser	Asp	Thr	Phe	Asp	Phe	Pro	Pro	Ala	Asp	Leu		
		280					285					290					
gcg	ctt	gct	cgt	ttg	tgc	gtc	gag	cgg	ggg	gcc	aca	gct	gct	cgg	tcc	1027	
Ala	Leu	Ala	Arg	Leu	Cys	Val	Glu	Arg	Gly	Ala	Thr	Ala	Ala	Arg	Ser		
		295				300					305						
acg	tca	gcg	cgc	ggg	gtg	att	gcg	ttg	gtt	gat	gcc	cat	cat	gcg	cac	1075	
Thr	Ser	Ala	Arg	Gly	Val	Ile	Ala	Leu	Val	Asp	Ala	His	His	Ala	His		
310					315					320					325		
aat	ttt	gct	gcg	gat	ctc	agc	gag	gat	ggc	ttg	ttg	gtg	gtt	cct	ctc	1123	
Asn	Phe	Ala	Ala	Asp	Leu	Ser	Glu	Asp	Gly	Leu	Leu	Val	Val	Pro	Leu		
				330				335						340			
ggg	cac	ggg	gac	gtc	gcg	gaa	cag	ggc	tagc	cgc	cct	act	ta	acc	cag	1170	
Gly	His	Gly	Asp	Val	Ala	Glu	Gln	Gly									
			345					350									
cct																	1173

&lt;210&gt; 486

&lt;211&gt; 350

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 486

Met Leu Leu Thr Tyr Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys  
 1 5 10 15  
 His Ser Leu Ser Thr Ala Asp Ile Ala Ala Arg Ala His Ala His Met  
 20 25 30  
 Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu  
 35 40 45  
 Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His  
 50 55 60  
 Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu  
 65 70 75 80  
 Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp  
 85 90 95  
 Val Ala Leu Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro  
 100 105 110  
 Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe  
 115 120 125  
 Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly  
 130 135 140  
 Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr  
 145 150 155 160  
 Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val  
 165 170 175  
 Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr  
 180 185 190  
 Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu  
 195 200 205  
 Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu  
 210 215 220  
 Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu  
 225 230 235 240  
 Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala  
 245 250 255  
 Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser  
 260 265 270  
 Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe  
 275 280 285  
 Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala  
 290 295 300  
 Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp

<400> 487																	
tagt	gtg	gcc	accta	aaacg	cgaac	aga	aac	cggag	tcgag	cagc	acctcc	ccgca	agggt	60			
agaggggctg cttttttgtt tcttaaattc accccatccc atg cat agc cct gaa 115																	
Met His Ser Pro Glu 5																	
agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163																	
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser 20																	
acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211																	
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr 35																	
gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259																	
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val 50																	
gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307																	
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp 65																	
cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355																	
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala 85																	
gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403																	
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp 100																	
cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451																	
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr 115																	
atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499																	
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr 130																	
tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547																	
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp 145																	

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac	595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn	
150 155 160 165	
agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct	643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala	
170 175 180	
cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct	691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser	
185 190 195	
atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca	739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala	
200 205 210	
gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc	787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr	
215 220 225	
tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac	835
Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn	
230 235 240 245	
tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca	883
Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala	
250 255 260	
gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc	931
Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu	
265 270 275	
atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag	979
Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln	
280 285 290	
gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa	1027
Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu	
295 300 305	
gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag	1075
Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln	
310 315 320 325	
aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg	1123
Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val	
330 335 340	
tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc	1171
Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile	
345 350 355	
gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca	1219
Asp Leu Leu Ala Glu Leu Ala Ala Val Arg Glu Arg Arg Ala Ala	
360 365 370	
gcc aag taattaaggg cgctagactg tta	1248
Ala Lys	
375	



&lt;210&gt; 488

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 488

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu  
 1 5 10 15

Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu  
 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys  
 35 40 45

Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe  
 50 55 60

Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val  
 65 70 75 80

His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu  
 85 90 95

Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe  
 100 105 110

Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro  
 115 120 125

His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg  
 130 135 140

Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu  
 145 150 155 160

Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp  
 165 170 175

Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu  
 180 185 190

Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly  
 195 200 205

Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His  
 210 215 220

Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr  
 225 230 235 240

Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly  
 245 250 255

Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly  
 260 265 270

Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys  
 275 280 285

Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile  
 290 295 300

Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu  
 305 310 315 320

Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly  
 325 330 335

Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp  
 340 345 350

Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg  
 355 360 365

Glu Arg Arg Ala Ala Ala Lys  
 370 375

<210> 489  
 <211> 1131  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1108)  
 <223> RXS02574

<400> 489  
 tgtgctcctt gcgggctgcg cagaagagcc ggaacagcaa aaagcaataa gccgcttattc 60

gacgtcccc tccaccctc ccgcaccgac cgcgaggat ttg gcg cgc gcg caa 115  
 Leu Ala Arg Ala Gln  
 1 5

atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163  
 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly  
 10 15 20

gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211  
 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly  
 25 30 35

ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259  
 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro  
 40 45 50

ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307  
 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser  
 55 60 65

gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355  
 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile  
 70 75 80 85

ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403  
 Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro  
 90 95 100

gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca 451

Glu	Gln	Val	Glu	Asp	Leu	Ala	Glu	Ile	Leu	Gly	Thr	Gly	Leu	Ala	Ala		
			105					110					115				
cat	ggg	gtg	aca	gtt	aac	ttt	gca	cct	gtt	gta	gat	gta	gat	gct	tgg	499	
His	Gly	Val	Thr	Val	Asn	Phe	Ala	Pro	Val	Val	Asp	Val	Asp	Ala	Trp		
		120					125					130					
ggg	ctc	ccc	gtc	gtt	ggc	gat	cgt	tcc	ttt	tcc	aac	gac	cca	gcc	gta	547	
Gly	Leu	Pro	Val	Val	Gly	Asp	Arg	Ser	Phe	Ser	Asn	Asp	Pro	Ala	Val		
		135				140					145						
gca	gct	act	tat	gcc	aca	gct	ttt	gca	aag	ggc	tta	agc	aaa	gta	gga	595	
Ala	Ala	Thr	Tyr	Ala	Thr	Ala	Phe	Ala	Lys	Gly	Leu	Ser	Lys	Val	Gly		
150					155					160					165		
att	acc	cca	gta	ttc	aaa	cat	ttc	cca	ggg	cac	ggg	cgt	gca	agt	ggc	643	
Ile	Thr	Pro	Val	Phe	Lys	His	Phe	Pro	Gly	His	Gly	Arg	Ala	Ser	Gly		
				170					175					180			
gat	tcg	cac	acc	caa	gat	gtg	gtg	acc	ccc	gca	ctt	gat	gag	ctt	aaa	691	
Asp	Ser	His	Thr	Gln	Asp	Val	Val	Thr	Pro	Ala	Leu	Asp	Glu	Leu	Lys		
			185					190					195				
act	tac	gac	ctc	atc	cct	tat	ggg	caa	gca	ctt	tct	gaa	act	gac	gga	739	
Thr	Tyr	Asp	Leu	Ile	Pro	Tyr	Gly	Gln	Ala	Leu	Ser	Glu	Thr	Asp	Gly		
		200					205					210					
gcc	gtc	atg	gtg	ggc	cac	atg	att	gtt	cca	ggg	ctt	ggc	acc	gac	gga	787	
Ala	Val	Met	Val	Gly	His	Met	Ile	Val	Pro	Gly	Leu	Gly	Thr	Asp	Gly		
		215				220					225						
gtt	cca	tcc	tct	atc	gac	ccc	gcc	acc	tat	caa	ctg	ctc	cgc	agt	ggc	835	
Val	Pro	Ser	Ser	Ile	Asp	Pro	Ala	Thr	Tyr	Gln	Leu	Leu	Arg	Ser	Gly		
230					235					240					245		
gat	tac	cca	ggg	ggc	gtg	cct	ttc	gat	ggc	gtg	atc	tac	acc	gac	gat	883	
Asp	Tyr	Pro	Gly	Gly	Val	Pro	Phe	Asp	Gly	Val	Ile	Tyr	Thr	Asp	Asp		
				250					255					260			
ctc	tct	gga	atg	agt	gcc	att	tcc	gcc	acc	cat	tca	ccc	gca	gaa	gca	931	
Leu	Ser	Gly	Met	Ser	Ala	Ile	Ser	Ala	Thr	His	Ser	Pro	Ala	Glu	Ala		
			265					270					275				
gtg	ctt	gcc	tcc	ctc	aaa	gca	ggc	gca	gac	caa	gca	cta	tgg	atc	gac	979	
Val	Leu	Ala	Ser	Leu	Lys	Ala	Gly	Ala	Asp	Gln	Ala	Leu	Trp	Ile	Asp		
		280					285					290					
tat	ggg	tcg	ttg	ggc	tcc	gcg	att	gat	cgc	gtt	gat	gct	gcc	gtt	agc	1027	
Tyr	Gly	Ser	Leu	Gly	Ser	Ala	Ile	Asp	Arg	Val	Asp	Ala	Ala	Val	Ser		
		295				300					305						
agc	ggg	gaa	tac	cct	caa	gaa	caa	atg	ctg	gca	tct	gcg	tta	aga	gtc	1075	
Ser	Gly	Glu	Tyr	Pro	Gln	Glu	Gln	Met	Leu	Ala	Ser	Ala	Leu	Arg	Val		
310					315					320					325		
caa	ttg	ctc	tac	atc	aca	cgt	ctc	gaa	caa	aag	tgaagttacc	agtcgtaac	1128				
Gln	Leu	Leu	Tyr	Ile	Thr	Arg	Leu	Glu	Gln	Lys							
				330					335								
ccc																	1131

<210> 490  
 <211> 336  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 490

```

Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser
 1             5             10             15

Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu
      20             25             30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn
      35             40             45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val
 50             55             60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln
 65             70             75             80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala
      85             90             95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly
      100            105            110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val
      115            120            125

Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser
      130            135            140

Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly
      145            150            155            160

Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
      165            170            175

Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala
      180            185            190

Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu
      195            200            205

Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly
      210            215            220

Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln
      225            230            235            240

Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val
      245            250            255

Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His
      260            265            270

Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln
      275            280            285

```

Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val  
 290 295 300

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala  
 305 310 315 320

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys  
 325 330 335

<210> 491  
 <211> 1038  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1008)  
 <223> RXS03215

<400> 491  
 atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc 48  
 Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
 1 5 10 15

gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca 96  
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
 20 25 30

ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc 144  
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
 35 40 45

cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc 192  
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
 50 55 60

cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag 240  
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
 65 70 75 80

ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga 288  
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
 85 90 95

tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc 336  
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
 100 105 110

tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa 384  
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
 115 120 125

ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc 432  
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
 130 135 140

acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac 480

Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
 145 150 155 160

gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac 528  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
 165 170 175

att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc 576  
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
 180 185 190

cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa 624  
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
 195 200 205

gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672  
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
 210 215 220

gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720  
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
 225 230 235 240

gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768  
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
 245 250 255

ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816  
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
 260 265 270

ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864  
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
 275 280 285

tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
 290 295 300

cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
 305 310 315 320

ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008  
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn  
 325 330 335

tagaaactat tcagaaagca tcaccatgaa 1038

&lt;210&gt; 492

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 492

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
 1 5 10 15

Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
 20 25 30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
           35                          40                          45  
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
           50                          55                          60  
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
           65                          70                          75                          80  
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
                           85                          90                          95  
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
                           100                          105                          110  
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
           115                          120                          125  
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
           130                          135                          140  
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
           145                          150                          155                          160  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
                           165                          170                          175  
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
                           180                          185                          190  
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
           195                          200                          205  
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
           210                          215                          220  
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
           225                          230                          235                          240  
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
                           245                          250                          255  
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
           260                          265                          270  
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
           275                          280                          285  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
           290                          295                          300  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
           305                          310                          315                          320  
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn  
                           325                          330                          335

<210> 493  
 <211> 1031  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1008)  
 <223> FRXA01915

<400> 493  
 atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc 48  
 Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
 1 5 10 15  
 gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca 96  
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
 20 25 30  
 ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc 144  
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
 35 40 45  
 cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc 192  
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
 50 55 60  
 cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag 240  
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
 65 70 75 80  
 ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga 288  
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
 85 90 95  
 tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc 336  
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
 100 105 110  
 tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa 384  
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
 115 120 125  
 ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc 432  
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
 130 135 140  
 acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac 480  
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
 145 150 155 160  
 gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac 528  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
 165 170 175  
 att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc 576  
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
 180 185 190  
 cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa 624



Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
 195 200 205  
 gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672  
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
 210 215 220  
 gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720  
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
 225 230 235 240  
 gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768  
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
 245 250 255  
 ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816  
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
 260 265 270  
 ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864  
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
 275 280 285  
 tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
 290 295 300  
 cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
 305 310 315 320  
 ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008  
 Gly Glu Thr Val Ala Val Pro Ala Ala Leu Ile Pro Ala Asn Asn  
 325 330 335  
 tagaaactat tcagaaagca tca 1031

&lt;210&gt; 494

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 494

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
 1 5 10 15  
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
 20 25 30  
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
 35 40 45  
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
 50 55 60  
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
 65 70 75 80  
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
 85 90 95

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
 100 105 110  
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
 115 120 125  
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
 130 135 140  
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
 145 150 155 160  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
 165 170 175  
 Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
 180 185 190  
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
 195 200 205  
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
 210 215 220  
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
 225 230 235 240  
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
 245 250 255  
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
 260 265 270  
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
 275 280 285  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
 290 295 300  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
 305 310 315 320  
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn  
 325 330 335

<210> 495  
 <211> 1288  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1258)  
 <223> RXS03224

<400> 495

acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgcaca 60

tggaactcat tgaacgccgc gcccggttaa ggtgggagggc atg agt ttt gct gaa 115  
Met Ser Phe Ala Glu  
1 5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163  
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro  
10 15 20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211  
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu  
25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259  
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met  
40 45 50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307  
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp  
55 60 65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355  
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala  
70 75 80 85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403  
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly  
90 95 100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451  
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr  
105 110 115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499  
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr  
120 125 130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547  
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu  
135 140 145

gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595  
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala  
150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643  
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro  
170 175 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691  
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr  
185 190 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739  
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys  
200 205 210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg 787  
Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp  
215 220 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca 835  
 Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr  
 230 235 240 245  
  
 ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa 883  
 Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln  
 250 255 260  
  
 tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc 931  
 Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr  
 265 270 275  
  
 cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979  
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu  
 280 285 290  
  
 gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027  
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu  
 295 300 305  
  
 ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075  
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile  
 310 315 320 325  
  
 gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123  
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val  
 330 335 340  
  
 ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171  
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly  
 345 350 355  
  
 ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219  
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg  
 360 365 370  
  
 atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268  
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala  
 375 380 385  
  
 ttcaagggtg ggggaacaaa 1288

&lt;210&gt; 496

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 496

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly  
 1 5 10 15  
  
 Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His  
 20 25 30  
  
 Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly  
 35 40 45  
  
 Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly  
 50 55 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu  
 65 70 75 80  
 Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly  
 85 90 95  
 Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr  
 100 105 110  
 Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala  
 115 120 125  
 Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val  
 130 135 140  
 Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala  
 145 150 155 160  
 Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val  
 165 170 175  
 Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly  
 180 185 190  
 Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu  
 195 200 205  
 Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe  
 210 215 220  
 Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr  
 225 230 235 240  
 Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala  
 245 250 255  
 Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe  
 260 265 270  
 Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe  
 275 280 285  
 Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro  
 290 295 300  
 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile  
 305 310 315 320  
 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln  
 325 330 335  
 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys  
 340 345 350  
 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu  
 355 360 365  
 Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr  
 370 375 380

Ser Ala  
385

<210> 497  
<211> 1281  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1258)  
<223> FRXA00038

<400> 497

```

acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgcaca 60
tggaactcat tgaacgccgc gcccggttaa ggtgggagggc atg agt ttt gct gaa 115
                                         Met Ser Phe Ala Glu
                                         1           5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
          10          15          20

atc cgg cct,gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
          25          30          35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
          40          45          50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
          55          60          65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
          70          75          80          85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
          90          95          100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
          105          110          115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
          120          125          130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
          135          140          145

gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
          150          155          160          165

```

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca	643
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro	
170 175 180	
cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac	691
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr	
185 190 195	
gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa	739
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys	
200 205 210	
gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg	787
Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp	
215 220 225	
act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca	835
Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr	
230 235 240 245	
ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa	883
Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln	
250 255 260	
tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc	931
Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr	
265 270 275	
cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag	979
Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu	
280 285 290	
gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag	1027
Asp Asn Val Phe Gly Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu	
295 300 305	
ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc	1075
Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile	
310 315 320 325	
gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc	1123
Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val	
330 335 340	
ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga	1171
Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly	
345 350 355	
ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg	1219
Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg	
360 365 370	
atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg	1268
Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala	
375 380 385	
ttcaagggta ggg	1281

&lt;210&gt; 498

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 498

```

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
 1           5           10           15

Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
      20           25           30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
      35           40           45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
      50           55           60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
      65           70           75           80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
      85           90           95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
      100           105           110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
      115           120           125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
      130           135           140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
      145           150           155           160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
      165           170           175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
      180           185           190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
      195           200           205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
      210           215           220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
      225           230           235           240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
      245           250           255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
      260           265           270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
      275           280           285

Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
      290           295           300

```



Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile  
 305 310 315 320

Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln  
 325 330 335

Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys  
 340 345 350

Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu  
 355 360 365

Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr  
 370 375 380

Ser Ala  
 385

<210> 499  
 <211> 517  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(517)  
 <223> RXC00233

<400> 499  
 cgcctccagc agttgaggga gaagttccaa cacttgacacc aactgaggaa gcaactgtgc 60

aatagcgctt tagacacaga ctcacgacag aatagaagac atg agt gtg aat gaa 115  
 Met Ser Val Asn Glu  
 1 5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163  
 Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly  
 10 15 20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211  
 Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val  
 25 30 35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259  
 Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr  
 40 45 50

tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307  
 Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val  
 55 60 65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355  
 Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu  
 70 75 80 85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403  
 Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg  
 90 95 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct 451

Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro  
 105 110 115

gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa 499  
 Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu  
 120 125 130

ggc cca cac cat ttc ctt 517  
 Gly Pro His His Phe Leu  
 135

<210> 500

<211> 139

<212> PRT

<213> Corynebacterium glutamicum

<400> 500

Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly  
 1 5 10 15

Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly  
 20 25 30

Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro  
 35 40 45

Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala  
 50 55 60

Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu  
 65 70 75 80

Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His  
 85 90 95

Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser  
 100 105 110

Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp  
 115 120 125

Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu  
 130 135

<210> 501

<211> 849

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(826)

<223> RXC00236

<400> 501

aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag ggggttagaaa 60

agcaatggga tttggatgcg gttcggtttt ggccgtcatc atg gtg atc tca ttt 115  
 Met Val Ile Ser Phe

	1	5	
gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa			163
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln			
	10	20	
ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt			211
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val			
	25	35	
ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt			259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg			
	40	50	
ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg			307
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala			
	55	65	
att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct			355
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro			
	70	85	
ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa			403
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu			
	90	100	
acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg			451
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu			
	105	115	
gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat			499
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp			
	120	130	
ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta			547
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu			
	135	145	
gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att			595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile			
	150	165	
ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta			643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val			
	170	180	
gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg			691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu			
	185	195	
ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca			739
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala			
	200	210	
gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga			787
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg			
	215	225	
gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa			836
Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile			
	230	240	

caagcgcaac ccc

849

&lt;210&gt; 502

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 502

Met Val Ile Ser Phe Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr  
 1 5 10 15

Ala Pro Ile Arg Gln Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala  
 20 25 30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr  
 35 40 45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly  
 50 55 60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala  
 65 70 75 80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly  
 85 90 95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe  
 100 105 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile  
 115 120 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr  
 130 135 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly  
 145 150 155 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala  
 165 170 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu  
 180 185 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro  
 195 200 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr  
 210 215 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro  
 225 230 235 240

Ala Ile

&lt;210&gt; 503

&lt;211&gt; 1113

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1090)

&lt;223&gt; RXC00271

&lt;400&gt; 503

tagttttaaat catgagacat ttcacatatg gttctttatc cgagacatgt gttgacgctg 60

tctgccccctt	tttgaaaata	acactttaag	gagatgtgcc	atg	ttt	tct	tcc	cgt	115
				Met	Phe	Ser	Ser	Arg	
				1				5	

tcg	aag	gta	ctc	gca	agc	atc	ttt	act	ggt	ggc	gcc	ttg	gcg	ttg	gct	163
Ser	Lys	Val	Leu	Ala	Ser	Ile	Phe	Thr	Val	Gly	Ala	Leu	Ala	Leu	Ala	
			10						15					20		

tcg	tgc	tca	agc	gat	tcc	agt	gac	agc	tcc	acc	tcc	act	gat	gct	gca	211
Ser	Cys	Ser	Ser	Asp	Ser	Ser	Asp	Ser	Ser	Thr	Ser	Thr	Asp	Ala	Ala	
			25				30						35			

ggt	ggc	gac	tct	tac	cga	ggt	ggc	atc	aac	cag	ctt	ggt	cag	cac	cct	259
Gly	Gly	Asp	Ser	Tyr	Arg	Val	Gly	Ile	Asn	Gln	Leu	Val	Gln	His	Pro	
		40					45					50				

gca	ctt	gat	gca	gcg	acc	act	ggt	ttc	aag	gaa	gct	ttt	gaa	gag	gca	307
Ala	Leu	Asp	Ala	Ala	Thr	Thr	Gly	Phe	Lys	Glu	Ala	Phe	Glu	Glu	Ala	
	55					60					65					

ggc	ggt	gac	gtc	acc	ttt	gat	gag	caa	aac	gct	aac	ggc	gag	cag	ggc	355
Gly	Val	Asp	Val	Thr	Phe	Asp	Glu	Gln	Asn	Ala	Asn	Gly	Glu	Gln	Gly	
	70				75				80					85		

act	gca	ctg	act	att	tct	cag	cag	ttc	gct	tct	gac	aat	ttg	gat	ctc	403
Thr	Ala	Leu	Thr	Ile	Ser	Gln	Gln	Phe	Ala	Ser	Asp	Asn	Leu	Asp	Leu	
			90					95						100		

gtg	ttg	gct	ggt	gca	act	cca	gca	gca	cag	gca	act	gcg	cag	aat	atc	451
Val	Leu	Ala	Val	Ala	Thr	Pro	Ala	Ala	Gln	Ala	Thr	Ala	Gln	Asn	Ile	
		105						110					115			

act	gat	atc	cca	gtc	ctg	ttc	acc	gca	ggt	acc	gat	gca	gtg	tcg	gca	499
Thr	Asp	Ile	Pro	Val	Leu	Phe	Thr	Ala	Val	Thr	Asp	Ala	Val	Ser	Ala	
		120				125					130					

gag	ctg	gtg	gat	tct	aat	gaa	gca	cct	ggc	gga	aac	gtc	acc	ggt	act	547
Glu	Leu	Val	Asp	Ser	Asn	Glu	Ala	Pro	Gly	Gly	Asn	Val	Thr	Gly	Thr	
	135					140					145					

tct	gat	atc	gca	ccg	att	gag	cag	cag	ttg	gag	ctt	ttg	cag	cag	ctg	595
Ser	Asp	Ile	Ala	Pro	Ile	Glu	Gln	Gln	Leu	Glu	Leu	Leu	Gln	Gln	Leu	
	150				155				160					165		

ggt	cct	gac	gca	aag	tcc	atc	ggc	atc	gtc	tac	gcg	tct	ggt	gag	gtc	643
Val	Pro	Asp	Ala	Lys	Ser	Ile	Gly	Ile	Val	Tyr	Ala	Ser	Gly	Glu	Val	
			170					175						180		

aac	tct	cag	gtg	cag	gtc	gat	gag	gtc	acc	aag	gct	gct	gag	cca	ctg	691
Asn	Ser	Gln	Val	Gln	Val	Asp	Glu	Val	Thr	Lys	Ala	Ala	Glu	Pro	Leu	

185	190	195	
ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag			739
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln			
200	205	210	
cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act			787
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr			
215	220	225	
gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag			835
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu			
230	235	240	245
cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt			883
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly			
250	255	260	
ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag			931
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln			
265	270	275	
act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca			979
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala			
280	285	290	
acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa			1027
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu			
295	300	305	
gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat			1075
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp			
310	315	320	325
aag gcc gaa cgc gta tgcacggcgc ttttgagttc gga			1113
Lys Ala Glu Arg Val			
330			

&lt;210&gt; 504

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 504

Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly		
1	5	10
Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr		
20	25	30
Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln		
35	40	45
Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu		
50	55	60
Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala		
65	70	75
Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser		

85							90							95						
Asp	Asn	Leu	Asp	Leu	Val	Leu	Ala	Val	Ala	Thr	Pro	Ala	Ala	Gln	Ala					
			100					105					110							
Thr	Ala	Gln	Asn	Ile	Thr	Asp	Ile	Pro	Val	Leu	Phe	Thr	Ala	Val	Thr					
		115					120					125								
Asp	Ala	Val	Ser	Ala	Glu	Leu	Val	Asp	Ser	Asn	Glu	Ala	Pro	Gly	Gly					
	130					135					140									
Asn	Val	Thr	Gly	Thr	Ser	Asp	Ile	Ala	Pro	Ile	Glu	Gln	Gln	Leu	Glu					
145					150					155					160					
Leu	Leu	Gln	Gln	Leu	Val	Pro	Asp	Ala	Lys	Ser	Ile	Gly	Ile	Val	Tyr					
				165					170					175						
Ala	Ser	Gly	Glu	Val	Asn	Ser	Gln	Val	Gln	Val	Asp	Glu	Val	Thr	Lys					
			180					185					190							
Ala	Ala	Glu	Pro	Leu	Gly	Leu	Ser	Val	Asn	Thr	Gln	Thr	Val	Thr	Thr					
		195					200					205								
Val	Asn	Glu	Ile	Gln	Gln	Ala	Val	Glu	Ala	Leu	Gly	Asp	Val	Asp	Val					
	210					215					220									
Ile	Tyr	Val	Pro	Thr	Asp	Asn	Met	Val	Val	Ser	Gly	Ile	Ser	Ser	Leu					
225					230					235					240					
Val	Gln	Val	Ala	Glu	Gln	Lys	Gln	Ile	Pro	Val	Ile	Gly	Ala	Glu	Ser					
				245					250					255						
Gly	Thr	Val	Glu	Gly	Gly	Ala	Leu	Ala	Thr	Leu	Gly	Ile	Asp	Tyr	Thr					
			260					265					270							
Glu	Leu	Gly	Arg	Gln	Thr	Gly	Glu	Met	Ala	Leu	Arg	Ile	Leu	Gln	Asp					
		275					280					285								
Gly	Glu	Asp	Pro	Ala	Thr	Met	Pro	Val	Glu	Thr	Ala	Thr	Glu	Phe	Thr					
	290					295					300									
Tyr	Val	Ile	Asn	Glu	Asp	Ala	Ala	Glu	Arg	Gln	Gly	Val	Glu	Ile	Pro					
305					310					315					320					
Gln	Glu	Ile	Leu	Asp	Lys	Ala	Glu	Arg	Val											
				325					330											

```
<210> 505
<211> 1263
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1240)  
<223> RXC00338
```

<400> 505  
tcttagaagg cgtagtcaca ccattaacct tqccagaatt tttcaaggct tggctagact 60

tgggaaacga acatgcggtg ccaaccaggg gagttaatgc	gtg agt gat gta acc	115
	Val Ser Asp Val Thr	
	1 5	
gtt ggc gat att cgc cgc att ttg gat gag gct tat ccg ccg gcg ttg	163	
Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu		
10 15 20		
gcg gaa agc tgg gac aaa gtg ggg ctg atc tgc ggt gat cca aca gag	211	
Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys Gly Asp Pro Thr Glu		
25 30 35		
tcg gtg aag cgt gtc ggt tta gca ctc gat tgc acc cag gca gtg gcc	259	
Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Val Ala		
40 45 50		
gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca	307	
Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro		
55 60 65		
ttg ctg ctg cgt ggg gtg acg tct gtt gct gcg gat gag cca aaa ggc	355	
Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala Asp Glu Pro Lys Gly		
70 75 80 85		
aag gtc att cac acc cta att cgc ggc ggg gtg gca ctg ttt tcc gcg	403	
Lys Val Ile His Thr Leu Ile Arg Gly Gly Val Ala Leu Phe Ser Ala		
90 95 100		
cac act aat gcg gat tcc gcg cgc cca ggt gtc aac gat aaa ctc gcc	451	
His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val Asn Asp Lys Leu Ala		
105 110 115		
gag ctc gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta	499	
Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu		
120 125 130		
ggc ggc atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg	547	
Gly Gly Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala		
135 140 145		
tac cta aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac	595	
Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp		
150 155 160 165		
tac cga gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc	643	
Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro		
170 175 180		
gtg gag ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa	691	
Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys		
185 190 195		
tcc ctt gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc	739	
Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala		
200 205 210		
cgg ctc acg tcg gtg ctg cgg gag gct cat ccg tat gag gag cct gcc	787	
Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala		
215 220 225		
ttc gat att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc	835	



Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr  
 230 235 240 245  
 gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat 883  
 Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp  
 250 255 260  
 ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg 931  
 Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val  
 265 270 275  
 cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca 979  
 Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser  
 280 285 290  
 tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg 1027  
 Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val  
 295 300 305  
 gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat 1075  
 Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr  
 310 315 320 325  
 ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc 1123  
 Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser  
 330 335 340  
 gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc 1171  
 Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala  
 345 350 355  
 cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc 1219  
 Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr  
 360 365 370  
 atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag 1263  
 Met Ser Ala Arg Ala Val Asn  
 375 380

&lt;210&gt; 506

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 506

Val Ser Asp Val Thr Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala  
 1 5 10 15  
 Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys  
 20 25 30  
 Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys  
 35 40 45  
 Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu  
 50 55 60  
 Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala  
 65 70 75 80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val  
                     85                    90                    95  
 Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val  
                     100                    105                    110  
 Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile  
                     115                    120                    125  
 Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu  
                     130                    135                    140  
 Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala  
                     145                    150                    155                    160  
 Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr  
                     165                    170                    175  
 Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val  
                     180                    185                    190  
 Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro  
                     195                    200                    205  
 Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro  
                     210                    215                    220  
 Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser  
                     225                    230                    235                    240  
 Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro  
                     245                    250                    255  
 Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val  
                     260                    265                    270  
 Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser  
                     275                    280                    285  
 Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val  
                     290                    295                    300  
 Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His  
                     305                    310                    315                    320  
 Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr  
                     325                    330                    335  
 Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile  
                     340                    345                    350  
 Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg  
                     355                    360                    365  
 Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn  
                     370                    375                    380

&lt;210&gt; 507

&lt;211&gt; 1470

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1447)

&lt;223&gt; RXC00362

&lt;400&gt; 507

```

cacttttttgg gtgaaaattc cacgaagtta atgccgcttt aagtcaattc aatcacatgt 60

aacatgctac gggttttttcg gtcacttaaa ggaggcgctt atg gga atc att gct 115
                                         Met Gly Ile Ile Ala
                                         1           5

ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa 163
Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
                        10                15                20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt 211
Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
                        25                30                35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat 259
Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
                        40                45                50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg 307
Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
                        55                60                65

ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc 355
Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
                        70                75                80                85

ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc 403
Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
                        90                95                100

act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga 451
Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
                        105                110                115

aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg 499
Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
                        120                125                130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc 547
Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly
                        135                140                145

ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca 595
Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala
                        150                155                160                165

ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg 643
Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu
                        170                175                180

gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt 691
Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe
                        185                190                195

```

tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg	739
Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg	
200 205 210	
gtg tca ttc ggt gag gca atg aag act gga tgg cgt tca ccg ttg atc	787
Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile	
215 220 225	
ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct	835
Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser	
230 235 240 245	
gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg	883
Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met	
250 255 260	
tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att	931
Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile	
265 270 275	
gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag	979
Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln	
280 285 290	
atc tcc aag gac ttg cca caa ttt gcc acc gta gga att tcg ttg ttt	1027
Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe	
295 300 305	
tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg	1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro	
310 315 320 325	
cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg	1123
Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met	
330 335 340	
gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg	1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser	
345 350 355	
tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg	1219
Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu	
360 365 370	
gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg	1267
Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu	
375 380 385	
tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac	1315
Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr	
390 395 400 405	
ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca	1363
Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro	
410 415 420	
ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt	1411
Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val	
425 430 435	

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta 1457  
 Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly  
 440 445

aaaatgaact caa 1470

<210> 508

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Met Gly Ile Ile Ala Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu  
 1 5 10 15

Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu  
 20 25 30

Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile  
 35 40 45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met  
 50 55 60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp  
 65 70 75 80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly  
 85 90 95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala  
 100 105 110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro  
 115 120 125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val  
 130 135 140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met  
 145 150 155 160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln  
 165 170 175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg  
 180 185 190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr  
 195 200 205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp  
 210 215 220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr  
 225 230 235 240

Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser  
 245 250 255

Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr  
 260 265 270  
 Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala  
 275 280 285  
 His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val  
 290 295 300  
 Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu  
 305 310 315 320  
 Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu  
 325 330 335  
 Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val  
 340 345 350  
 Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro  
 355 360 365  
 Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile  
 370 375 380  
 Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val  
 385 390 395 400  
 Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr  
 405 410 415  
 Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu  
 420 425 430  
 Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr  
 435 440 445

Gly

<210> 509  
 <211> 1203  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1180)  
 <223> RXC00412

<400> 509  
 cttttgacga acaccacgtc gcgtacgctt cctcggggcg ttaaactatt tgtcttccag 60  
 cttttgtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115  
 Val Ser His Thr Ala  
 1 5  
 tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163  
 Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln  
 10 15 20

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat	211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn	
25 30 35	
aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa	259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu	
40 45 50	
ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc gcc aag tcc	307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser	
55 60 65	
act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg	355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser	
70 75 80 85	
ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg	403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu	
90 95 100	
cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg	451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu	
105 110 115	
ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt	499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val	
120 125 130	
gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc	547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu	
135 140 145	
gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg	595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu	
150 155 160 165	
tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc	643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr	
170 175 180	
aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca	691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro	
185 190 195	
gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa	739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu	
200 205 210	
ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt	787
Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg	
215 220 225	
tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa	835
Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu	
230 235 240 245	
tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct	883
Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala	
250 255 260	
caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa	931

Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu  
 265 270 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979  
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu  
 280 285 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027  
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln  
 295 300 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075  
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg  
 310 315 320 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123  
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala  
 330 335 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171  
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu  
 345 350 355

atc acc cga tgaacgagat gatacctcgca gct 1203  
 Ile Thr Arg  
 360

&lt;210&gt; 510

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 510

Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln  
 1 5 10 15

Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys  
 20 25 30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val  
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser  
 50 55 60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser  
 65 70 75 80

Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met  
 85 90 95

Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe  
 100 105 110

Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu  
 115 120 125

Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg  
 130 135 140



```

<400> 511
gggtggagcag gcggcggtct cttttagtcc tgcgggccct tttgaccctg cagcccctgc 60

cgtttctgcc aagcaaaccg tggggcaggt gatttagcct atg agc ctc atc gaa 115
                                     Met Ser Leu Ile Glu
                                     1           5

atg cga aat att qtc aaq acc tac aac att gga tct gaa ggt gaa ctc 163

```

Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly Ser Glu Gly Glu Leu  
10 15 20

acc gtg ttg cac ggt gtg gat ttc cat gtg gac cgt ggc gaa ttc gtg 211  
Thr Val Leu His Gly Val Asp Phe His Val Asp Arg Gly Glu Phe Val  
25 30 35

tcg gtt gtg ggt acg tcc ggc tca ggt aaa tca acg atg atg aac atc 259  
Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser Thr Met Met Asn Ile  
40 45 50

att ggg ttg ttg gat aag cca act gat ggc acg tac acc ttg gat ggc 307  
Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr Tyr Thr Leu Asp Gly  
55 60 65

gtg gat gtg ttg gat atc agc gat gat gct ttg gcg agc cac cgc gct 355  
Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu Ala Ser His Arg Ala  
70 75 80 85

aaa tcg att ggt ttt gtg ttt cag aac ttc aat ctg att ggc cgg atc 403  
Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn Leu Ile Gly Arg Ile  
90 95 100

gat gcg ttg aag aat gtg gaa atg ccc atg atg tat gcg ggc att ccg 451  
Asp Ala Leu Lys Asn Val Glu Met Pro Met Met Tyr Ala Gly Ile Pro  
105 110 115

gct aag cag cgg aga agt cgt gcg gtt gaa tta ttg gaa atg gtc ggg 499  
Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu Leu Glu Met Val Gly  
120 125 130

atg ggt gag cgt ctc aac cat gag ccc aat gag ctt tcg ggt ggt cag 547  
Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu Leu Ser Gly Gly Gln  
135 140 145

aag cag cgc gtg gcc att gct cgc gcg ttg gcg aac gat cct gag atc 595  
Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala Asn Asp Pro Glu Ile  
150 155 160 165

att ctt gct gat gaa cca act ggt gcg ttg gat tct gca acg ggc cgg 643  
Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp Ser Ala Thr Gly Arg  
170 175 180

atg gtg atg gat att ttc cac cag ctc aac aag gag cag ggc aaa acc 691  
Met Val Met Asp Ile Phe His Gln Leu Asn Lys Glu Gln Gly Lys Thr  
185 190 195

atc gtg ttt att act cac aac cct gag ctt gct gat gaa tct gat cgg 739  
Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala Asp Glu Ser Asp Arg  
200 205 210

gtg gtc acc atg gtt gac ggg cgc atc att ggg tct gag gtg aaa cac 787  
Val Val Thr Met Val Asp Gly Arg Ile Ile Gly Ser Glu Val Lys His  
215 220 225

tca tgagccttgc agaatcaatt ctt 813  
Ser  
230

&lt;210&gt; 512

<211> 230  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 512

```

Met Ser Leu Ile Glu Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly
  1           5           10           15

Ser Glu Gly Glu Leu Thr Val Leu His Gly Val Asp Phe His Val Asp
      20           25           30

Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser
      35           40           45

Thr Met Met Asn Ile Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr
  50           55           60

Tyr Thr Leu Asp Gly Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu
  65           70           75           80

Ala Ser His Arg Ala Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn
      85           90           95

Leu Ile Gly Arg Ile Asp Ala Leu Lys Asn Val Glu Met Pro Met Met
      100          105          110

Tyr Ala Gly Ile Pro Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu
      115          120          125

Leu Glu Met Val Gly Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu
      130          135          140

Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala
      145          150          155          160

Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp
      165          170          175

Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys
      180          185          190

Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala
      195          200          205

Asp Glu Ser Asp Arg Val Val Thr Met Val Asp Gly Arg Ile Ile Gly
      210          215          220

Ser Glu Val Lys His Ser
      225          230

```

<210> 513  
 <211> 1185  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1162)  
 <223> RXC01004

&lt;400&gt; 513

```

ccggacgctg gatcgacacga gtaacggtca tggaagatcg acgcatcgac aaagccgttc 60

tcacccccat cacccatgaa gaagcaaagg agtacgaaaa gtg agt att tgg gca 115
                                   Val Ser Ile Trp Ala
                                   1 5

act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg 163
Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
                                   10 15 20

gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc 211
Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
                                   25 30 35

ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc 259
Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
                                   40 45 50

gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307
Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
                                   55 60 65

tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc 355
Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
                                   70 75 80 85

att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac 403
Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His
                                   90 95 100

cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att 451
Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile
                                   105 110 115

ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct ggc cct gaa 499
Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu
                                   120 125 130

acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att 547
Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile
                                   135 140 145

acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt 595
Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu
                                   150 155 160 165

cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac 643
Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp
                                   170 175 180

cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa ggc ctc 691
Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu
                                   185 190 195

ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag 739
Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu
                                   200 205 210

cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg 787
Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr

```

215	220	225	
ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca			835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala			
230	235	240	245
gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga			883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly			
250	255		260
tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct			931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala			
265	270		275
gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc			979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg			
280	285		290
cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat			1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp			
295	300		305
ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt			1075
Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly			
310	315		320
gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg			1123
Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val			
330	335		340
ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt			1172
Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp			
345	350		
aactgtgttg gac			1185

&lt;210&gt; 514

&lt;211&gt; 354

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 514

Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala
1 5 10 15

Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg
20 25 30

Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
35 40 45

Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
50 55 60

Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
65 70 75 80

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
85 90 95

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile  
 100 105 110  
 Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala  
 115 120 125  
 Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile  
 130 135 140  
 Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile  
 145 150 155 160  
 Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu  
 165 170 175  
 Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser  
 180 185 190  
 Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys  
 195 200 205  
 Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp  
 210 215 220  
 Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His  
 225 230 235 240  
 Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val  
 245 250 255  
 Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile  
 260 265 270  
 Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro  
 275 280 285  
 Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met  
 290 295 300  
 Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln  
 305 310 315 320  
 Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu  
 325 330 335  
 Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser  
 340 345 350  
 Asp Asp

&lt;210&gt; 515

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(709)

&lt;223&gt; RXC01017

&lt;400&gt; 515

gaaatttgag ggggcgctac ccttagaagg tgcgcaatga caccacgata gttcgcgcct 60

agtgtggatt gctagaaaac tttaagaaag aggaaataat atg gct caa aaa gta 115  
 Met Ala Gln Lys Val  
 1 5

acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc 163  
 Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg  
 10 15 20

tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt 211  
 Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val  
 25 30 35

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat 259  
 Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp  
 40 45 50

tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca 307  
 Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala  
 55 60 65

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca 355  
 Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala  
 70 75 80 85

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc 403  
 Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser  
 90 95 100

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct 451  
 Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala  
 105 110 115

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc 499  
 Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg  
 120 125 130

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547  
 Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr  
 135 140 145

cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc 595  
 Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr  
 150 155 160 165

cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc 643  
 Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe  
 170 175 180

aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691  
 Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr  
 185 190 195

gag aac cca cag ttc gac taattaacgc tgtctctgct tat 732  
 Glu Asn Pro Gln Phe Asp  
 200

<210> 516  
 <211> 203  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 516

```

Met Ala Gln Lys Val Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys
 1           5           10           15

Trp Val Thr Ser Arg Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile
          20           25           30

Glu Ile Gln Trp Val Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg
          35           40           45

Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro
          50           55           60

Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly
          65           70           75           80

Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly
          85           90           95

Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu
          100          105          110

Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp
          115          120          125

Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly
          130          135          140

Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe
          145          150          155          160

Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile
          165          170          175

Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile
          180          185          190

Lys Arg Ser Arg Thr Glu Asn Pro Gln Phe Asp
          195          200

```

<210> 517  
 <211> 622  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXC01021

<400> 517

```

cgagaggctt ttttggtctt aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115
Met Ser Ser Ser Glu

```



	1	5	
agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa			163
Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu			
	10	15	20
cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct			211
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala			
	25	30	35
tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct			259
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala			
	40	45	50
gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc			307
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val			
	55	60	65
ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg			355
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met			
	70	75	80
aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc			403
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val			
	90	95	100
gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga			451
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg			
	105	110	115
gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag			499
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln			
	120	125	130
gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta			547
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu			
	135	140	145
tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag			595
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu			
	150	155	160
ggc act gtt gtc act gtg ttg cgt tct			622
Gly Thr Val Val Thr Val Leu Arg Ser			
	170		

&lt;210&gt; 518

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 518

Met	Ser	Ser	Ser	Glu	Ser	Ser	Arg	Ser	Glu	Gly	Ser	Gln	Pro	Ala	Pro
1				5					10					15	

Ser	Val	Gln	Pro	Glu	Arg	Arg	Ala	Asp	Ser	Thr	Gly	Ala	Pro	Ala	Ala
			20					25					30		

Ala	Ser	Lys	Glu	Ala	Ser	Gln	Gln	Met	Asp	Ala	Ala	Gly	Val	Leu	Glu
		35					40					45			

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile  
 50 55 60  
 Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn  
 65 70 75 80  
 Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly  
 85 90 95  
 Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser  
 100 105 110  
 Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu  
 115 120 125  
 Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr  
 130 135 140  
 Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile  
 145 150 155 160  
 Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser  
 165 170

<210> 519  
 <211> 1047  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1024)  
 <223> RXC01212

<400> 519  
 tttagaagcc acatgacata tgtcatgaaa attatgtgca aagtgcagta atactcctga 60

catatggctc taccagcgcc aatgcgaagt aggaagaatt atg cct atg aca acg 115  
 Met Pro Met Thr Thr  
 1 5

aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac 163  
 Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr  
 10 15 20

acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt 211  
 Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe  
 25 30 35

ggt ctg ctc ggc acc aac ggg gcc ggc aaa acc tcc acc ttg gaa gtc 259  
 Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val  
 40 45 50

atc gaa gga ctt tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg 307  
 Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly  
 55 60 65

ctt gac ccc gtt gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc 355  
 Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile

70	75	80	85	
atg ctg caa tca ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc				403
Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr				
	90	95	100	
atg gac atg tgg cac ggc acc tgc acg tat ccg cgc gcc att aaa gat				451
Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp				
	105	110	115	
gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc				499
Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly				
	120	125	130	
gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg				547
Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu				
	135	140	145	
ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc				595
Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu				
	150	155	160	
gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa				643
Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys				
	170	175	180	
cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc				691
Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala				
	185	190	195	
gaa ttc ctc tgc gac cgg att gcc atc atg aac gcc ggt gag atc gca				739
Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala				
	200	205	210	
gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc				787
Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile				
	215	220	225	
agt ttc gtg ctg cgt ggc ggg cag gtg gag ttg ccg gtc ttg agt ggg				835
Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly				
	230	235	240	245
gct gaa atc atc cgc gac aac aac cac gtc cgc atc gcc acc acc acc				883
Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr				
	250	255	260	
ctg cag cag cac acc tta gaa ata ctt acc tgg gct gca gag acc ggg				931
Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly				
	265	270	275	
atc gcg ctg gaa ggc ttc gct gca aaa ccc gcc acc ttg gaa tcc gta				979
Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val				
	280	285	290	
ttc atg gac atc gcc tca ctc gag aac acc tcg ctg caa acc gcc				1024
Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser Leu Gln Thr Ala				
	295	300	305	
tagaatcttt aaggagacca caa				1047

<210> 520  
 <211> 308  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 520

Met	Pro	Met	Thr	Thr	Thr	Pro	Ala	Ile	Asp	Val	Thr	Asp	Leu	Val	Arg
1				5					10					15	
Thr	Tyr	Gly	Asp	Tyr	Thr	Ala	Val	Lys	Gly	Leu	Asn	Phe	His	Val	Gln
			20					25					30		
Arg	Gly	Glu	Val	Phe	Gly	Leu	Leu	Gly	Thr	Asn	Gly	Ala	Gly	Lys	Thr
		35					40					45			
Ser	Thr	Leu	Glu	Val	Ile	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Ser	Gly	Thr
	50					55					60				
Val	Arg	Ile	Ser	Gly	Leu	Asp	Pro	Val	Ala	Asp	Arg	Ala	Ile	Leu	Arg
65					70					75					80
Pro	Glu	Leu	Gly	Ile	Met	Leu	Gln	Ser	Gly	Gly	Leu	Pro	Ser	Gln	Leu
				85					90					95	
Thr	Val	Ala	Glu	Thr	Met	Asp	Met	Trp	His	Gly	Thr	Cys	Thr	Tyr	Pro
			100					105					110		
Arg	Ala	Ile	Lys	Asp	Val	Leu	Ala	Asp	Val	Asp	Leu	Leu	His	Arg	Glu
		115					120					125			
Asn	Val	Lys	Val	Gly	Ala	Leu	Ser	Gly	Gly	Glu	Gln	Arg	Arg	Leu	Asp
	130						135				140				
Leu	Ala	Cys	Ala	Leu	Leu	Gly	Asp	Pro	Ser	Ile	Leu	Phe	Leu	Asp	Glu
145					150					155					160
Pro	Thr	Thr	Gly	Leu	Asp	Pro	Glu	Ser	Arg	Arg	His	Thr	Trp	Gln	Leu
				165					170					175	
Leu	Leu	Asp	Leu	Lys	Gln	Arg	Gly	Val	Thr	Met	Met	Leu	Thr	Thr	His
			180					185					190		
Tyr	Leu	Glu	Glu	Ala	Glu	Phe	Leu	Cys	Asp	Arg	Ile	Ala	Ile	Met	Asn
		195					200					205			
Ala	Gly	Glu	Ile	Ala	Val	Glu	Gly	Thr	Leu	Asp	Glu	Leu	Val	Ala	Arg
	210					215					220				
Glu	Lys	Ser	Ile	Ile	Ser	Phe	Val	Leu	Arg	Gly	Gly	Gln	Val	Glu	Leu
225					230					235					240
Pro	Val	Leu	Ser	Gly	Ala	Glu	Ile	Ile	Arg	Asp	Asn	Asn	His	Val	Arg
				245					250					255	
Ile	Ala	Thr	Thr	Thr	Leu	Gln	Gln	His	Thr	Leu	Glu	Ile	Leu	Thr	Trp
			260					265					270		
Ala	Ala	Glu	Thr	Gly	Ile	Ala	Leu	Glu	Gly	Phe	Ala	Ala	Lys	Pro	Ala
		275					280					285			
Thr	Leu	Glu	Ser	Val	Phe	Met	Asp	Ile	Ala	Ser	Leu	Glu	Asn	Thr	Ser

290

295

300

Leu Gln Thr Ala  
305

&lt;210&gt; 521

&lt;211&gt; 1131

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1108)

&lt;223&gt; RXC01306

&lt;400&gt; 521

tggttttagag gtagagcgaa acgtgcctgt aaaactggcg ctcgctgtgc tcgaagacca 60

cccagacaat caccocgctc cgaaggagaa tcgctaagcc atg act gaa tgg tat 115  
Met Thr Glu Trp Tyr  
1 5

gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc 163  
Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe  
10 15 20

gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag 211  
Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu  
25 30 35

gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc 259  
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu  
40 45 50

aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg 307  
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met  
55 60 65

gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct 355  
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala  
70 75 80 85

ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat 403  
Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp  
90 95 100

gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg 451  
Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu  
105 110 115

gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag 499  
Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu  
120 125 130

acg gca ctt cga act atc gcg att ccc gca cgg ggc ttc att aac ctg 547  
Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu  
135 140 145

ttt cgt cca ttg ctg cag tgg atc aac aaa atg gcg aac gat ttg gtc 595  
Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met Ala Asn Asp Leu Val

150	155	160	165	
cgc aaa gtt ggt gaa act ccc gtt gat cga gct gca gct ggt ggc tat				643
Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala Ala Ala Gly Gly Tyr				
	170	175	180	
gac acc gat acc ctc cat gcc ctc att gag cat tcc cga gaa act ggc				691
Asp Thr Asp Thr Leu His Ala Leu Ile Glu His Ser Arg Glu Thr Gly				
	185	190	195	
gct ctg gat cag caa tcc gcc gcc caa atc agc gga att atc aag ctg				739
Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser Gly Ile Ile Lys Leu				
	200	205	210	
gat aaa atc acg gtc ggt caa acc ctg acc gca tct cca ttt acg cac				787
Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala Ser Pro Phe Thr His				
	215	220	225	
agc gcc agc gcc acg gtt gct gag gtg caa gcc gca gct cag cgc agt				835
Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala Ala Ala Gln Arg Ser				
	230	235	240	245
ggc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac				883
Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His				
	250	255	260	
gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct				931
Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala				
	265	270	275	
tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta				979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu				
	280	285	290	
cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg				1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala				
	295	300	305	
gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat				1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp				
	310	315	320	325
cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct				1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val				
	330	335		
gaa				1131
<210> 522				
<211> 336				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 522				
Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala				
1	5	10	15	
Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg				
20	25	30		

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala  
 35 40 45  
 Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln  
 50 55 60  
 Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro  
 65 70 75 80  
 Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro  
 85 90 95  
 Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val  
 100 105 110  
 Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala  
 115 120 125  
 Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg  
 130 135 140  
 Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met  
 145 150 155 160  
 Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala  
 165 170 175  
 Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His  
 180 185 190  
 Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser  
 195 200 205  
 Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala  
 210 215 220  
 Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala  
 225 230 235 240  
 Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser  
 245 250 255  
 His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser  
 260 265 270  
 Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala  
 275 280 285  
 Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn  
 290 295 300  
 Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly  
 305 310 315 320  
 Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val  
 325 330 335

```

<400> 524
Val Ser Gln Phe Arg Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala
  1             5             10             15

```



Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly  
 20 25 30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His  
 35 40 45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val  
 50 55 60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln  
 65 70 75 80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp  
 85 90 95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu  
 100 105 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp  
 115 120 125

Glu Ser  
 130

<210> 525  
 <211> 614  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(591)  
 <223> RXC01372

<400> 525  
 cag gac acc ttc gtc ctt ccc acc ttg ccc acg gcc gca ggc ttg tcg 48  
 Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser  
 1 5 10 15

cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa 96  
 Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu  
 20 25 30

gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc 144  
 Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys  
 35 40 45

att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc 192  
 Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val  
 50 55 60

aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg 240  
 Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val  
 65 70 75 80

cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc 288  
 His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala  
 85 90 95

cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc 336

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro  
 100 105 110

gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc 384  
 Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr  
 115 120 125

gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta 432  
 Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val  
 130 135 140

ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat 480  
 Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp  
 145 150 155 160

gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa 528  
 Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln  
 165 170 175

gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att 576  
 Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile  
 180 185 190

gaa gaa aag gac ttg taaatggagc tattggaagg ctc 614  
 Glu Glu Lys Asp Leu  
 195

&lt;210&gt; 526

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 526

Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser  
 1 5 10 15

Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu  
 20 25 30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys  
 35 40 45

Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val  
 50 55 60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val  
 65 70 75 80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala  
 85 90 95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro  
 100 105 110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr  
 115 120 125

Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val  
 130 135 140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp  
 145 150 155 160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln  
 165 170 175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile  
 180 185 190

Glu Glu Lys Asp Leu  
 195

<210> 527  
 <211> 669  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(646)  
 <223> RXC01659

<400> 527  
 ttgatgcgcg ccgcggtgag cagcctgccg atccagagcg tgaagaatct gatgatttag 60

tcgagattga taccgtctct ggattccgcc tgctcagtag gtg gcg ggg gtt gcg 115  
 Val Ala Gly Val Ala  
 1 5

cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca 163  
 Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro  
 10 15 20

gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa 211  
 Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu  
 25 30 35

acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg 259  
 Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro  
 40 45 50

ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg 307  
 Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr  
 55 60 65

cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag 355  
 Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys  
 70 75 80 85

ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa 403  
 Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu  
 90 95 100

gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg 451  
 Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met  
 105 110 115

ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca 499  
 Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser  
 120 125 130

ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt 547  
 Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg  
 135 140 145  
 ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag 595  
 Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln  
 150 155 160 165  
 tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag 643  
 Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys  
 170 175 180  
 tgg tagaaaactg gtgttttttcg gcc 669  
 Trp

&lt;210&gt; 528

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 528

Val Ala Gly Val Ala Gln Arg Phe Val Asp Glu Arg Ile His Val Gly  
 1 5 10 15  
 Leu Asp Ser Met Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp  
 20 25 30  
 Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu  
 35 40 45  
 Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu  
 50 55 60  
 Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu  
 65 70 75 80  
 Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro  
 85 90 95  
 Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu  
 100 105 110  
 Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val  
 115 120 125  
 Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu  
 130 135 140  
 Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg  
 145 150 155 160  
 Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp  
 165 170 175  
 Glu Pro Pro Lys Lys Trp  
 180

<210> 529  
 <211> 981  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(958)  
 <223> RXC01663

<400> 529

```
tattttgctg gttggtcaca gtggagcgct aaccccgaga atcctatcga ggcctaaaat 60

cgtggcttga gtacgcactg ccagtaagggt gtgtgatgtg atg gaa ata agt gtc 115
                               Met Glu Ile Ser Val
                               1 5

ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc 163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
                10                15                20

gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc 211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
                25                30                35

tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag 259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
                40                45                50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag 307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
                55                60                65

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag 355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
                70                75                80                85

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat 403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
                90                95                100

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac 451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
                105                110                115

ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg 499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
                120                125                130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat aag cat tcg ttt 547
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe
                135                140                145

ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg 595
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala
                150                155                160                165

gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat 643
Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp
                170                175                180
```

gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg 691  
 Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val  
 185 190 195  
  
 gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg 739  
 Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala  
 200 205 210  
  
 ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc 787  
 Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val  
 215 220 225  
  
 att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa 835  
 Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu  
 230 235 240 245  
  
 tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc 883  
 Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu  
 250 255 260  
  
 agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg 931  
 Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr  
 265 270 275  
  
 tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa 978  
 Ser Val Trp Ile Pro Cys Gln Lys Leu  
 280 285  
  
 tct 981

&lt;210&gt; 530

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 530

Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly  
 1 5 10 15  
  
 Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala  
 20 25 30  
  
 Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu  
 35 40 45  
  
 Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala  
 50 55 60  
  
 Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro  
 65 70 75 80  
  
 Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp  
 85 90 95  
  
 Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr  
 100 105 110  
  
 Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln  
 115 120 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val  
 130 135 140

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu  
 145 150 155 160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp  
 165 170 175

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala  
 180 185 190

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His  
 195 200 205

Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile  
 210 215 220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp  
 225 230 235 240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser  
 245 250 255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser  
 260 265 270

Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu  
 275 280 285

&lt;210&gt; 531

&lt;211&gt; 1545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1522)

&lt;223&gt; RXC01693

&lt;400&gt; 531

aggagactgg ctggattatt ggctggtttt cttgggaaat cgtcatgggc attaatccta 60

gtcccaacaa ttgccagaac ccgaacacta ggcttgaacc atg aat act gca cct 115  
 Met Asn Thr Ala Pro  
 1 5

ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc 163  
 Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala  
 10 15 20

ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat 211  
 Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn  
 25 30 35

gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca 259  
 Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr  
 40 45 50

cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca 307

Pro	Glu	Gly	Val	Gln	Phe	Leu	Leu	Gly	Leu	Asn	Pro	Glu	Pro	Leu	Thr		
	55					60				65							
aaa	gca	gtt	gcg	cag	gcc	tat	tcc	ggc	cac	caa	ttc	gga	cag	ttt	gtg	355	
Lys	Ala	Val	Ala	Gln	Ala	Tyr	Ser	Gly	His	Gln	Phe	Gly	Gln	Phe	Val		
	70				75				80						85		
gca	agc	ctt	ggt	gat	ggc	cga	gcg	ctt	ctt	ctc	ggc	gaa	gcc	cgc	tca	403	
Ala	Ser	Leu	Gly	Asp	Gly	Arg	Ala	Leu	Leu	Leu	Gly	Glu	Ala	Arg	Ser		
				90				95						100			
gct	gac	ggc	gta	ctg	cat	gat	atc	cac	ctc	aaa	gga	tct	gga	cga	acc	451	
Ala	Asp	Gly	Val	Leu	His	Asp	Ile	His	Leu	Lys	Gly	Ser	Gly	Arg	Thr		
			105				110						115				
caa	ttc	tcc	cga	gga	gcc	gat	gga	cgc	gcc	gtc	ctt	ggc	ccc	gtc	tta	499	
Gln	Phe	Ser	Arg	Gly	Ala	Asp	Gly	Arg	Ala	Val	Leu	Gly	Pro	Val	Leu		
		120					125					130					
cgc	gaa	tac	atc	atc	tcc	gaa	gcg	atg	cat	gca	ctt	ggt	ggt	ccc	acc	547	
Arg	Glu	Tyr	Ile	Ile	Ser	Glu	Ala	Met	His	Ala	Leu	Gly	Val	Pro	Thr		
	135					140					145						
acc	agg	tca	ctt	gca	gta	att	agc	acc	ggt	agg	aaa	atc	caa	cga	gga	595	
Thr	Arg	Ser	Leu	Ala	Val	Ile	Ser	Thr	Gly	Arg	Lys	Ile	Gln	Arg	Gly		
	150				155					160					165		
agc	gta	gcc	cca	ggc	gca	gtc	ctt	gtt	cga	gta	gca	acc	agc	ctc	att	643	
Ser	Val	Ala	Pro	Gly	Ala	Val	Leu	Val	Arg	Val	Ala	Thr	Ser	Leu	Ile		
				170					175					180			
cga	gtc	gga	tcc	ttc	caa	tac	tcc	aac	atc	tct	ggt	ggc	atc	gaa	cta	691	
Arg	Val	Gly	Ser	Phe	Gln	Tyr	Ser	Asn	Ile	Ser	Gly	Gly	Ile	Glu	Leu		
			185					190					195				
tct	caa	cac	ctg	gcg	aac	tat	acg	atc	acc	agg	cat	ttc	cct	tcg	ttg	739	
Ser	Gln	His	Leu	Ala	Asn	Tyr	Thr	Ile	Thr	Arg	His	Phe	Pro	Ser	Leu		
		200					205					210					
gta	gct	gaa	cta	tcc	gca	cca	acc	ccc	gca	act	tat	gta	tca	ctg	ttt	787	
Val	Ala	Glu	Leu	Ser	Ala	Pro	Thr	Pro	Ala	Thr	Tyr	Val	Ser	Leu	Phe		
	215					220					225						
aaa	gcg	att	ctt	cag	cgc	caa	gca	gac	acc	gtt	gga	aaa	tgg	acc	agg	835	
Lys	Ala	Ile	Leu	Gln	Arg	Gln	Ala	Asp	Thr	Val	Gly	Lys	Trp	Thr	Arg		
	230				235				240						245		
ctg	ggt	ttc	gtt	cac	gga	gcc	ctc	aac	aca	gac	aac	acg	ttg	ata	tcc	883	
Leu	Gly	Phe	Val	His	Gly	Ala	Leu	Asn	Thr	Asp	Asn	Thr	Leu	Ile	Ser		
				250				255						260			
gga	gaa	act	gtt	gac	tac	ggc	cca	tgc	gct	ttc	atg	gag	cgc	tac	cgt	931	
Gly	Glu	Thr	Val	Asp	Tyr	Gly	Pro	Cys	Ala	Phe	Met	Glu	Arg	Tyr	Arg		
			265				270						275				
ggc	gac	gcg	aaa	ttt	agc	tcc	atc	gac	act	tat	ggt	cgc	tac	aaa	ttt	979	
Gly	Asp	Ala	Lys	Phe	Ser	Ser	Ile	Asp	Thr	Tyr	Gly	Arg	Tyr	Lys	Phe		
		280					285					290					
gaa	aac	caa	cct	atg	atc	ctc	gga	tgg	aac	atg	gcc	cgc	ctc	gta	gaa	1027	
Glu	Asn	Gln	Pro	Met	Ile	Leu	Gly	Trp	Asn	Met	Ala	Arg	Leu	Val	Glu		



295                      300                      305  
 acc ctc ctc cca ctc ctg ggc gcc aca cca gac gaa ggc atg aca gca 1075  
 Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp Glu Gly Met Thr Ala  
 310                      315                      320                      325  
 gcc caa gaa gct ctc gta gaa ttc gat gac ctc tgc gaa caa gca atc 1123  
 Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu Cys Glu Gln Ala Ile  
 330                      335                      340  
 cga aaa gaa ttc gcc act gca ctg ggc ctt gac gag tca gac acc ggc 1171  
 Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp Glu Ser Asp Thr Gly  
 345                      350                      355  
 acg gta gag cag ttc cgt gaa ctg ctc tac ctc cat aac ccc gac atc 1219  
 Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu His Asn Pro Asp Ile  
 360                      365                      370  
 acc acg ctg ctg cgc gca ctc acc gac aac acc gca cca ccg agt ggc 1267  
 Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr Ala Pro Pro Ser Gly  
 375                      380                      385  
 ttt gaa gca ttc gtt cac gac tgg aaa acc caa gac cca gat atc gaa 1315  
 Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln Asp Pro Asp Ile Glu  
 390                      395                      400                      405  
 gca atg cga gca gta aat cca ctt ttc att cca cgc aat cac ctc gtg 1363  
 Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro Arg Asn His Leu Val  
 410                      415                      420  
 gaa gct gct ctc gca gac gca gtt gaa ggg aat cta gaa aag ttc cac 1411  
 Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn Leu Glu Lys Phe His  
 425                      430                      435  
 gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc 1459  
 Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro  
 440                      445                      450  
 gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg 1507  
 Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met  
 455                      460                      465  
 acc ttc tgc ggt acc taggacagat ggtggggcag acg 1545  
 Thr Phe Cys Gly Thr  
 470

&lt;210&gt; 532

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 532

Met Asn Thr Ala Pro Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu  
 1                      5                      10                      15

Pro Thr Met Ala Ala Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu  
 20                      25                      30

Leu Val Ile Leu Asn Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro  
 35                      40                      45

Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn  
 50 55 60  
 Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln  
 65 70 75 80  
 Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu  
 85 90 95  
 Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys  
 100 105 110  
 Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val  
 115 120 125  
 Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala  
 130 135 140  
 Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg  
 145 150 155 160  
 Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val  
 165 170 175  
 Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser  
 180 185 190  
 Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg  
 195 200 205  
 His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr  
 210 215 220  
 Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val  
 225 230 235 240  
 Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp  
 245 250 255  
 Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe  
 260 265 270  
 Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr  
 275 280 285  
 Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met  
 290 295 300  
 Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp  
 305 310 315 320  
 Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu  
 325 330 335  
 Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp  
 340 345 350  
 Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu  
 355 360 365

His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr  
 370 375 380  
 Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln  
 385 390 395 400  
 Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro  
 405 410 415  
 Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn  
 420 425 430  
 Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp  
 435 440 445  
 Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe  
 450 455 460  
 Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr  
 465 470

<210> 533  
 <211> 1236  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1213)  
 <223> RXC01703

<400> 533  
 gttagacaaa tgggtaaaca gagctgacct agcgggaatcc gccatcaacg aaaggcattc 60  
 cgcgagggtt tggggctctgc ctcgaacaaa tcttggggtt gtg gca tgg cca tcc 115  
 Val Ala Trp Pro Ser  
 1 5  
 aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg 163  
 Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala  
 10 15 20  
 cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag 211  
 His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys  
 25 30 35  
 gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc 259  
 Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg  
 40 45 50  
 aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg 307  
 Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp  
 55 60 65  
 ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca 355  
 Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr  
 70 75 80 85  
 cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat 403  
 Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp

90										95				100				
tcc	ctt	act	ggt	gtg	ctg	ccg	tgg	cgt	tcc	ggc	gaa	acc	ttc	tac	aac	451		
Ser	Leu	Thr	Gly	Val	Leu	Pro	Trp	Arg	Ser	Gly	Glu	Thr	Phe	Tyr	Asn			
			105				110						115					
gtt	ccc	tcc	aac	ggt	cct	gct	gcg	atc	atg	atg	gcc	cgc	acc	gac	cgt	499		
Val	Pro	Ser	Asn	Gly	Pro	Ala	Ala	Ile	Met	Met	Ala	Arg	Thr	Asp	Arg			
			120				125						130					
ttg	gac	gag	gct	atg	aaa	atc	acc	gat	tgg	att	ttt	gac	aac	ctg	atc	547		
Leu	Asp	Glu	Ala	Met	Lys	Ile	Thr	Asp	Trp	Ile	Phe	Asp	Asn	Leu	Ile			
			135				140						145					
gat	ggc	gac	ggc	ctt	gtg	atg	gac	gga	ttg	cgc	atg	cgc	atg	cac	gga	595		
Asp	Gly	Asp	Gly	Leu	Val	Met	Asp	Gly	Leu	Arg	Met	Arg	Met	His	Gly			
			150				155						160					
cct	gag	ctt	gtc	cgt	tcc	atc	cac	ccg	tat	tgc	caa	ggg	gtc	gcc	att	643		
Pro	Glu	Leu	Val	Arg	Ser	Ile	His	Pro	Tyr	Cys	Gln	Gly	Val	Ala	Ile			
			170				175						180					
ggt	gcg	tgt	ttg	gaa	att	gct	ctc	aaa	ctg	cgt	gag	cgc	gca	ggc	ttg	691		
Gly	Ala	Cys	Leu	Glu	Ile	Ala	Leu	Lys	Leu	Arg	Glu	Arg	Ala	Gly	Leu			
			185				190						195					
acc	act	act	gtg	gtg	gat	cac	tgg	tcg	gat	gcc	gat	aag	gca	gaa	gac	739		
Thr	Thr	Thr	Val	Val	Asp	His	Trp	Ser	Asp	Ala	Asp	Lys	Ala	Glu	Asp			
			200				205						210					
tcc	ctc	aaa	tac	ttt	gca	cac	atc	cac	gct	gtg	gtt	cag	gct	gtg	tcg	787		
Ser	Leu	Lys	Tyr	Phe	Ala	His	Ile	His	Ala	Val	Val	Gln	Ala	Val	Ser			
			215				220						225					
cgg	aag	atg	acc	aac	ttc	cac	ggc	gtt	att	gat	tgg	gac	acc	ggg	gac	835		
Arg	Lys	Met	Thr	Asn	Phe	His	Gly	Val	Ile	Asp	Trp	Asp	Thr	Gly	Asp			
			230				235						240					
ggc	gac	ggc	ggg	ttg	ttc	aag	ggc	att	ttg	gtc	cgc	tat	tta	gct	gat	883		
Gly	Asp	Gly	Gly	Leu	Phe	Lys	Gly	Ile	Leu	Val	Arg	Tyr	Leu	Ala	Asp			
			250				255						260					
gtg	gcc	atc	cgc	ctg	cct	gac	gat	tca	cca	acc	aac	cgg	gaa	acc	aaa	931		
Val	Ala	Ile	Arg	Leu	Pro	Asp	Asp	Ser	Pro	Thr	Asn	Arg	Glu	Thr	Lys			
			265				270						275					
aag	att	gca	gca	cgc	ctg	gta	ctg	gaa	tcg	gcg	gaa	agc	gta	tgg	aac	979		
Lys	Ile	Ala	Ala	Arg	Leu	Val	Leu	Glu	Ser	Ala	Glu	Ser	Val	Trp	Asn			
			280				285						290					
cac	cga	ttg	gaa	gtt	gat	ggc	ctt	ccg	gta	ttc	gcc	aca	gac	tgg	aca	1027		
His	Arg	Leu	Glu	Val	Asp	Gly	Leu	Pro	Val	Phe	Ala	Thr	Asp	Trp	Thr			
			295				300						305					
acg	gat	gca	cgc	ctg	cca	caa	aac	ttt	ggg	ttg	agt	tcc	tct	agt	ttg	1075		
Thr	Asp	Ala	Arg	Leu	Pro	Gln	Asn	Phe										

caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa 1171  
 Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu  
                   345                  350                  355

gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga 1213  
 Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg  
                   360                  365                  370

tagccccgat agtgtatgtg ctg 1236

<210> 534

<211> 371

<212> PRT

<213> Corynebacterium glutamicum

<400> 534

Val Ala Trp Pro Ser Asn Ala Lys Glu Lys Leu Phe Ile His Trp His  
   1                  5                  10                  15

Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg  
                   20                  25                  30

Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg  
                   35                  40                  45

Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr  
                   50                  55                  60

Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val  
   65                  70                  75                  80

Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile  
                   85                  90                  95

Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly  
                   100                  105                  110

Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met  
                   115                  120                  125

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile  
                   130                  135                  140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg  
   145                  150                  155                  160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys  
                   165                  170                  175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg  
                   180                  185                  190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala  
                   195                  200                  205

Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val  
   210                  215                  220

Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp

225                      230                      235                      240  
 Trp Asp Thr Gly Asp Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val  
                                  245                      250                      255  
 Arg Tyr Leu Ala Asp Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr  
                                  260                      265                      270  
 Asn Arg Glu Thr Lys Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala  
                                  275                      280                      285  
 Glu Ser Val Trp Asn His Arg Leu Glu Val Asp Gly Leu Pro Val Phe  
                                  290                      295                      300  
 Ala Thr Asp Trp Thr Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu  
                                  305                      310                      315                      320  
 Ser Ser Ser Ser Leu Ser Asp Leu Val Ser Val Val Arg Val Asp Glu  
                                  325                      330                      335  
 Arg Asp Leu Ser Val Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala  
                                  340                      345                      350  
 Ala Lys Val Ala Glu Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly  
                                  355                      360                      365  
 Arg Ser Arg  
                                  370

&lt;210&gt; 535

&lt;211&gt; 800

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(777)

&lt;223&gt; RXC02254

&lt;400&gt; 535

atc gcc gtt gcc gaa gaa ggc gga ttg tgg gaa aac ctc ctg cag cac      48  
 Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His  
   1                      5                      10                      15  
 cgc ttc ggt gga cat ggt gcg cta gct ggt cac gcc ttg gga aac ctc      96  
 Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu  
                                  20                      25                      30  
 gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt      144  
 Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu  
                                  35                      40                      45  
 gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta      192  
 Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val  
                                  50                      55                      60  
 tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct      240  
 Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser  
   65                      70                      75                      80

gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca 288  
 Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala  
 85 90 95

acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa 336  
 Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu  
 100 105 110

ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc 384  
 Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr  
 115 120 125

ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc 432  
 Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val  
 130 135 140

cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg 480  
 Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val  
 145 150 155 160

gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca 528  
 Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala  
 165 170 175

gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt 576  
 Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val  
 180 185 190

gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc 624  
 Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg  
 195 200 205

aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc 672  
 Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe  
 210 215 220

cat gat gtc cag gct gaa gat ggc cgt ggt cga ttc acc agt att cac 720  
 His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His  
 225 230 235 240

gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca 768  
 Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala  
 245 250 255

cga aag cgt taaggagtag gcgtgtcact gac 800  
 Arg Lys Arg

&lt;210&gt; 536

&lt;211&gt; 259

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 536

Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His  
 1 5 10 15

Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu  
 20 25 30

```

<400> 537
gtgtgcagcg ttgctggcaa gttttgctgg agcacgaaag cgттаaggag taggcgtgtc 60
actgacgagt gatatcaaac aagaattggc gcaggtccat gtg gcc aaa aac agt 115
                                     Val Ala Lys Asn Ser

```



															1	5	
gtt	cgt	gct	gcg	gaa	gtg	tct	gca	att	tta	agg	ttt	gct	ggt	gag	atg	163	
Val	Arg	Ala	Ala	Glu	Val	Ser	Ala	Ile	Leu	Arg	Phe	Ala	Gly	Glu	Met		
				10					15					20			
caa	gct	gtc	ggc	ggc	aag	ctg	gtc	atc	gaa	gca	aat	ttg	gac	agc	atg	211	
Gln	Ala	Val	Gly	Gly	Lys	Leu	Val	Ile	Glu	Ala	Asn	Leu	Asp	Ser	Met		
				25					30					35			
caa	gtc	ggg	atg	agg	ctt	cag	gag	ttt	atc	caa	ggg	ttg	tac	aac	tct	259	
Gln	Val	Gly	Met	Arg	Leu	Gln	Glu	Phe	Ile	Gln	Gly	Leu	Tyr	Asn	Ser		
				40					45					50			
cga	gtc	gat	gtg	cac	acc	gtg	aac	ccg	act	gtg	agc	agg	aaa	acg	cca	307	
Arg	Val	Asp	Val	His	Thr	Val	Asn	Pro	Thr	Val	Ser	Arg	Lys	Thr	Pro		
				55					60					65			
cgg	tat	ttg	gtg	cgc	atc	att	gac	aat	gcc	gat	gaa	att	gcg	cga	cgc	355	
Arg	Tyr	Leu	Val	Arg	Ile	Ile	Asp	Asn	Ala	Asp	Glu	Ile	Ala	Arg	Arg		
				70					75					80			
acc	gga	ctg	gtc	acc	agg	tct	gga	cat	gtg	gtt	aaa	ggg	cta	gcg	cct	403	
Thr	Gly	Leu	Val	Thr	Arg	Ser	Gly	His	Val	Val	Lys	Gly	Leu	Ala	Pro		
				90					95					100			
tct	gtg	gtc	agc	gga	aca	atc	agt	gac	gct	gaa	gct	gca	tgg	cgc	ggg	451	
Ser	Val	Val	Ser	Gly	Thr	Ile	Ser	Asp	Ala	Glu	Ala	Ala	Trp	Arg	Gly		
				105					110					115			
gcg	ttt	cta	gcc	aat	gga	tct	tta	agt	gat	cca	ggg	cgt	tcc	tct	tcg	499	
Ala	Phe	Leu	Ala	Asn	Gly	Ser	Leu	Ser	Asp	Pro	Gly	Arg	Ser	Ser	Ser		
				120					125					130			
ttg	gag	gtg	ttg	tgt	cct	ggg	caa	gaa	tca	gca	ttg	gca	ctg	gtt	gga	547	
Leu	Glu	Val	Leu	Cys	Pro	Gly	Gln	Glu	Ser	Ala	Leu	Ala	Leu	Val	Gly		
				135					140					145			
tgt	gcg	cga	aga	att	ggg	atc	gcg	gcg	aaa	acg	aaa	gat	tct	cga	gga	595	
Cys	Ala	Arg	Arg	Ile	Gly	Ile	Ala	Ala	Lys	Thr	Lys	Asp	Ser	Arg	Gly		
				150					155					160			
ttt	gat	cgc	gtc	aat	gtt	cgt	gat	gcg	gaa	gca	att	ggg	gca	ctg	ctc	643	
Phe	Asp	Arg	Val	Asn	Val	Arg	Asp	Ala	Glu	Ala	Ile	Gly	Ala	Leu	Leu		
				170					175					180			
act	cga	atg	ggg	gcc	cag	aaa	act	cgc	atg	ttg	tgg	gaa	gaa	aaa	cgc	691	
Thr	Arg	Met	Gly	Ala	Gln	Lys	Thr	Arg	Met	Leu	Trp	Glu	Glu	Lys	Arg		
				185					190					195			
atc	aag	cgg	gaa	agt	cga	act	ccg	caa	acc	ggg	ttg	gcc	aac	ttc	gac	739	
Ile	Lys	Arg	Glu	Ser	Arg	Thr	Pro	Gln	Thr	Gly	Leu	Ala	Asn	Phe	Asp		
				200					205					210			
gat	gcc	aat	ctg	cgc	agg	tca	gcc	cga	gca	gca	gtt	gcc	gct	gca	gcg	787	
Asp	Ala	Asn	Leu	Arg	Arg	Ser	Ala	Arg	Ala	Ala	Val	Ala	Ala	Ala	Ala		
				215					220					225			
agg	gta	gaa	cgc	gcc	atg	aag	att	ctt	ggg	gat	gat	gtt	cct	gag	cat	835	
Arg	Val	Glu	Arg	Ala	Met	Lys	Ile	Leu	Gly	Asp	Asp	Val	Pro	Glu	His		
				230					235					240			

ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg 883  
 Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu  
                   250                                  255                                  260  
  
 gag gag ttg ggc cgg ttg gct gat cct caa atg acc aag gat gct gtg 931  
 Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val  
                   265                                  270                                  275  
  
 gcc ggt cgt att cgt cgt ctt ttg acg atg gca gat aag cgc gcc gaa 979  
 Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu  
                   280                                  285                                  290  
  
 gat ctg aag att cct gat aca aat tct gtt gtg acg gaa gat ttg ttg 1027  
 Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val Thr Glu Asp Leu Leu  
                   295                                  300                                  305  
  
 gaa gaa att tagatgattg aagcctaaaa acg 1059  
 Glu Glu Ile  
 310

&lt;210&gt; 538

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 538

Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg  
   1                                  5                                  10                                  15  
  
 Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala  
                   20                                  25                                  30  
  
 Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln  
                   35                                  40                                  45  
  
 Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val  
                   50                                  55                                  60  
  
 Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp  
                   65                                  70                                  75                                  80  
  
 Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val  
                                   85                                  90                                  95  
  
 Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu  
                   100                                  105                                  110  
  
 Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro  
                   115                                  120                                  125  
  
 Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala  
                   130                                  135                                  140  
  
 Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr  
                   145                                  150                                  155                                  160  
  
 Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala  
                   165                                  170                                  175

Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu  
 180 185 190

Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly  
 195 200 205

Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala  
 210 215 220

Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp  
 225 230 235 240

Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His  
 245 250 255

Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met  
 260 265 270

Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala  
 275 280 285

Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val  
 290 295 300

Thr Glu Asp Leu Leu Glu Glu Ile  
 305 310

<210> 539  
 <211> 681  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(658)  
 <223> RXC02435

<400> 539  
 tcatgaatgt agaacggatt tatcgacaag cgccagcaag tacgttgatc tcttttagcca 60

tcatcgctgt gtacgcagtg cggccattca atcgagatca gtg aca gac aac ctg 115  
 Val Thr Asp Asn Leu  
 1 5

ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163  
 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met  
 10 15 20

gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211  
 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu  
 25 30 35

cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259  
 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu  
 40 45 50

ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg 307  
 Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala  
 55 60 65

atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg 355  
 Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met  
 70 75 80 85  
 gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg 403  
 Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met  
 90 95 100  
 atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga 451  
 Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg  
 105 110 115  
 gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc 499  
 Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser  
 120 125 130  
 acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct 547  
 Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala  
 135 140 145  
 tta att act tgg cca atg gtt aaa gcg aaa act caa aga aca cgg tgg 595  
 Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp  
 150 155 160 165  
 att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta 643  
 Ile Ile Val Leu Ile Gly Phe Ala Val Val Val Ala Ala Val Ile Leu  
 170 175 180  
 gga att gac cgg gtg tagacacatt ccgcccattg ccc 681  
 Gly Ile Asp Arg Val  
 185

&lt;210&gt; 540

&lt;211&gt; 186

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 540

Val Thr Asp Asn Leu Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu  
 1 5 10 15  
 Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile  
 20 25 30  
 Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu  
 35 40 45  
 Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser  
 50 55 60  
 Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala  
 65 70 75 80  
 Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly  
 85 90 95  
 Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg  
 100 105 110  
 Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala

115	120	125
Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly		
130	135	140
Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr		
145	150	155
Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val		
165	170	175
Ala Ala Val Ile Leu Gly Ile Asp Arg Val		
180	185	

&lt;210&gt; 541

&lt;211&gt; 681

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(658)

&lt;223&gt; FRXA02435

&lt;400&gt; 541

tcataaatgt agaacggatt tatcgacaag cgccagcaag tacgttgatc tcttttagcca 60

tcatacgtgt gtacgcagtg cggccattca atcgagatca gtg aca gac aac ctg	115
Val Thr Asp Asn Leu	
1 5	

ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg	163
Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met	
10 15 20	

gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg	211
Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu	
25 30 35	

cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg	259
His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu	
40 45 50	

ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg	307
Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala	
55 60 65	

atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg	355
Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met	
70 75 80 85	

gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg	403
Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met	
90 95 100	

atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga	451
Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg	
105 110 115	

gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc	499
---	-----

Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser  
 120 125 130

acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct 547  
 Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala  
 135 140 145

tta att act tgg cca atg gtt aaa gcg aaa act caa aga aca cgg tgg 595  
 Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp  
 150 155 160 165

att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta 643  
 Ile Ile Val Leu Ile Gly Phe Ala Val Val Val Ala Ala Val Ile Leu  
 170 175 180

gga att gac cgg gtg tagacacatt ccgcccattg ccc 681  
 Gly Ile Asp Arg Val  
 185

&lt;210&gt; 542

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 542

Val Thr Asp Asn Leu Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu  
 1 5 10 15

Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile  
 20 25 30

Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu  
 35 40 45

Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser  
 50 55 60

Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala  
 65 70 75 80

Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly  
 85 90 95

Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg  
 100 105 110

Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala  
 115 120 125

Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly  
 130 135 140

Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr  
 145 150 155 160

Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val  
 165 170 175

Ala Ala Val Ile Leu Gly Ile Asp Arg Val  
 180 185

<210> 543  
<211> 1141  
<212> DNA  
<213> Corynebacterium glutamicum

```
<220>  
<221> CDS  
<222> (101)..(1111)  
<223> RXC03216
```

<400> 543																
gctgtatcac agtcagctgc agcaggtggc gaaaccgttg cgggtcccagc ggctgctctg 60																
atccctgcaa acaactagaa actattcaga aagcatcacc atg aaa ctc ggt ctc 115																
Met Lys Leu Gly Leu 5																
1																
tac aac gcg atc ttc cac gac cgc acc ctg cca gaa gcg ctc gca gcc 163																
Tyr Asn Ala Ile Phe His Asp Arg Thr Leu Pro Glu Ala Leu Ala Ala 20																
10 15																
atc aaa gct gca ggt ctc acc gga att gaa ctc aac acc ggc gga ttt 211																
Ile Lys Ala Ala Gly Leu Thr Gly Ile Glu Leu Asn Thr Gly Gly Phe 35																
25 30																
ttg cct gca acc cac atc ccg acc atc gat gac atc ctg gtc agc gat 259																
Leu Pro Ala Thr His Ile Pro Thr Ile Asp Asp Ile Leu Val Ser Asp 50																
40 45																
gat gcc cgc gat gaa ttc ctc ggg att ttc gaa ggc acc ggc gtc gac 307																
Asp Ala Arg Asp Glu Phe Leu Gly Ile Phe Glu Gly Thr Gly Val Asp 65																
55 60																
atc tac ggc ctt aac tgc aac ggc aac ccg ctt cac ccc aac aag gcg 355																
Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu His Pro Asn Lys Ala 85																
70 75 80																
atc ggg gac aag cat gcc gaa gac att cga cgt tcc atc cgc ctc gca 403																
Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg Ser Ile Arg Leu Ala 100																
90 95																
gag cgc ctc ggc caa aac cgt gtg gtc acc atg tct ggt ctt cct ggt 451																
Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met Ser Gly Leu Pro Gly 115																
105 110																
ggc gaa cca ggc gcg aag tac acc aac tgg gtt gtc aac gcg tgg aac 499																
Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val Val Asn Ala Trp Asn 130																
120 125																
tcc gca gcc ttg gat gtc ctt gat tac caa tgg gat atc gca gct gaa 547																
Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp Asp Ile Ala Ala Glu 145																
135 140																
ttc tgg cgc gag acc gac cgc ttc gcc gca gat cac ggc gtg aaa gtg 595																
Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp His Gly Val Lys Val 165																
150 155 160																
gct ctt gag ctg cac cca cag aac atc gtg ttc aac tcc gct gac gtg 643																
Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe Asn Ser Ala Asp Val																

170	175	180	
cat aag ctc atc gat ctc acc ggc gcc acc cac gtg ggc gtc gaa ctg			691
His Lys Leu Ile Asp Leu Thr Gly Ala Thr His Val Gly Val Glu Leu			
185	190	195	
gat gca tca cac ctg ttc tgg cag cag atg gac cca atc gct gtg att			739
Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp Pro Ile Ala Val Ile			
200	205	210	
gat cac ctc ggc gag ctc atc ttc cac gcc gcc gcc aaa gac gtg cga			787
Asp His Leu Gly Glu Leu Ile Phe His Ala Ala Ala Lys Asp Val Arg			
215	220	225	
gtt aat aag gaa tgg gct cag ctc aac ggt gtg ctg gac aac agc ttc			835
Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val Leu Asp Asn Ser Phe			
230	235	240	245
cga cgc ctt gac cca tcc gaa aac cgc acc aac ttg ggc ggc gac gag			883
Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn Leu Gly Gly Asp Glu			
250	255	260	
tgg gcg aat gaa tgg cca aag aac tct gct tgg gat ttc gtt gct ctg			931
Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp Asp Phe Val Ala Leu			
265	270	275	
ggc cgc ggt cat gac gtt gct tac tgg acc gaa ttc ctc cgc gca ctt			979
Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu Phe Leu Arg Ala Leu			
280	285	290	
cac cgc gtc gat cca aac atg ctg gtc aac atc gaa cac gag gat gtt			1027
His Arg Val Asp Pro Asn Met Leu Val Asn Ile Glu His Glu Asp Val			
295	300	305	
tca ctc ggt cgc gaa gaa ggc gtc aac gaa gcc gct aag gtg ctg atc			1075
Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala Ala Lys Val Leu Ile			
310	315	320	325
gag gcc aac aag gca ctc gaa gag tcc ctg gtt tct taaaaaaaaact			1121
Glu Ala Asn Lys Ala Leu Glu Glu Ser Leu Val Ser			
330	335		
acgcctgccc cgcaacgctt			1141

&lt;210&gt; 544

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 544

Met	Lys	Leu	Gly	Leu	Tyr	Asn	Ala	Ile	Phe	His	Asp	Arg	Thr	Leu	Pro
1				5					10					15	

Glu	Ala	Leu	Ala	Ala	Ile	Lys	Ala	Ala	Gly	Leu	Thr	Gly	Ile	Glu	Leu
			20					25					30		

Asn	Thr	Gly	Gly	Phe	Leu	Pro	Ala	Thr	His	Ile	Pro	Thr	Ile	Asp	Asp
		35					40					45			

Ile	Leu	Val	Ser	Asp	Asp	Ala	Arg	Asp	Glu	Phe	Leu	Gly	Ile	Phe	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



50					55					60					
Gly	Thr	Gly	Val	Asp	Ile	Tyr	Gly	Leu	Asn	Cys	Asn	Gly	Asn	Pro	Leu
65					70					75					80
His	Pro	Asn	Lys	Ala	Ile	Gly	Asp	Lys	His	Ala	Glu	Asp	Ile	Arg	Arg
				85					90					95	
Ser	Ile	Arg	Leu	Ala	Glu	Arg	Leu	Gly	Gln	Asn	Arg	Val	Val	Thr	Met
			100					105					110		
Ser	Gly	Leu	Pro	Gly	Gly	Glu	Pro	Gly	Ala	Lys	Tyr	Thr	Asn	Trp	Val
		115					120					125			
Val	Asn	Ala	Trp	Asn	Ser	Ala	Ala	Leu	Asp	Val	Leu	Asp	Tyr	Gln	Trp
		130					135					140			
Asp	Ile	Ala	Ala	Glu	Phe	Trp	Arg	Glu	Thr	Asp	Arg	Phe	Ala	Ala	Asp
145							150					155			160
His	Gly	Val	Lys	Val	Ala	Leu	Glu	Leu	His	Pro	Gln	Asn	Ile	Val	Phe
				165					170					175	
Asn	Ser	Ala	Asp	Val	His	Lys	Leu	Ile	Asp	Leu	Thr	Gly	Ala	Thr	His
			180					185					190		
Val	Gly	Val	Glu	Leu	Asp	Ala	Ser	His	Leu	Phe	Trp	Gln	Gln	Met	Asp
		195					200					205			
Pro	Ile	Ala	Val	Ile	Asp	His	Leu	Gly	Glu	Leu	Ile	Phe	His	Ala	Ala
	210						215					220			
Ala	Lys	Asp	Val	Arg	Val	Asn	Lys	Glu	Trp	Ala	Gln	Leu	Asn	Gly	Val
225							230					235			240
Leu	Asp	Asn	Ser	Phe	Arg	Arg	Leu	Asp	Pro	Ser	Glu	Asn	Arg	Thr	Asn
				245					250					255	
Leu	Gly	Gly	Asp	Glu	Trp	Ala	Asn	Glu	Trp	Pro	Lys	Asn	Ser	Ala	Trp
			260					265					270		
Asp	Phe	Val	Ala	Leu	Gly	Arg	Gly	His	Asp	Val	Ala	Tyr	Trp	Thr	Glu
	275						280					285			
Phe	Leu	Arg	Ala	Leu	His	Arg	Val	Asp	Pro	Asn	Met	Leu	Val	Asn	Ile
	290						295				300				
Glu	His	Glu	Asp	Val	Ser	Leu	Gly	Arg	Glu	Glu	Gly	Val	Asn	Glu	Ala
305							310					315			320
Ala	Lys	Val	Leu	Ile	Glu	Ala	Asn	Lys	Ala	Leu	Glu	Glu	Ser	Leu	Val
				325					330					335	

Ser

&lt;210&gt; 545

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1393)

&lt;223&gt; RXA02175

&lt;400&gt; 545

```

tgacatgcgc ttggcgcac ccagtttgta agaataaacg ggactacttc cgtaatccgg 60

aagagttttt ttccgaacaa atatgtttga aagggatatc gtg gct act gat aac 115
                               Val Ala Thr Asp Asn
                               1 5

aac aag gct gtc ctg cac tac ccc ggt ggc gag ttc gaa atg gac atc 163
Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile
                               10 15 20

atc gag gct tct gag ggt aac aac ggt gtt gtc ctg ggc aag atg ctg 211
Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu
                               25 30 35

tct gag act gga ctg atc act ttt gac cca ggt tat gtg agc act ggc 259
Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly
                               40 45 50

tcc acc gag tcg aag atc acc tac atc gat ggc gat gcg gga atc ctg 307
Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu
                               55 60 65

cgt tac cgc ggc tat gac atc gct gat ctg gct gag aat gcc acc ttc 355
Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe
                               70 75 80 85

aac gag gtt tct tac cta ctt atc aac ggt gag cta cca acc cca gat 403
Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp
                               90 95 100

gag ctt cac aag ttt aac gac gag att cgc cac cac acc ctt ctg gac 451
Glu Leu His Lys Phe Asn Asp Glu Ile Arg His His Thr Leu Leu Asp
                               105 110 115

gag gac ttc aag tcc cag ttc aac gtg ttc cca cgc gac gct cac cca 499
Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro
                               120 125 130

atg gca acc ttg gct tcc tcg gtt aac att ttg tct acc tac tac cag 547
Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln
                               135 140 145

gac cag ctg aac cca ctc gat gag gca cag ctt gat aag gca acc gtt 595
Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val
                               150 155 160 165

cgc ctc atg gca aag gtt cca atg ctg gct gcg tac gca cac cgc gca 643
Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala
                               170 175 180

cgc aag ggt gct cct tac atg tac cca gac aac tcc ctc aat gcg cgt 691
Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg
                               185 190 195

```

gag aac ttc ctg cgc atg atg ttc ggt tac cca acc gag cca tac gag	739
Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu	
200 205 210	
atc gac cca atc atg gtc aag gct ctg gac aag ctg ctc atc ctg cac	787
Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His	
215 220 225	
gct gac cac gag cag aac tgc tcc acc tcc acc gtt cgt atg atc ggt	835
Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly	
230 235 240 245	
tcc gca cag gcc aac atg ttt gtc tcc atc gct ggt ggc atc aac gct	883
Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala	
250 255 260	
ctg tcc ggc cca ctg cac ggt ggc gca aac cag gct gtt ctg gag atg	931
Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln Ala Val Leu Glu Met	
265 270 275	
ctc gaa gac atc aag agc aac cac ggt ggc gac gca acc gag ttc atg	979
Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp Ala Thr Glu Phe Met	
280 285 290	
aac aag gtc aag aac aag gaa gac ggc gtc cgc ctc atg ggc ttc gga	1027
Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly	
295 300 305	
cac cgc gtt tac aag aac tac gat cca cgt gca gca atc gtc aag gag	1075
His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu	
310 315 320 325	
acc gca cac gag atc ctc gag cac ctc ggt ggc gac gat ctt ctg gat	1123
Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp	
330 335 340	
ctg gca atc aag ctg gaa gaa att gca ctg gct gat gat tac ttc atc	1171
Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile	
345 350 355	
tcc cgc aag ctc tac ccg aac gta gac ttc tac acc ggc ctg atc tac	1219
Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr	
360 365 370	
cgc gca atg ggc ttc cca act gac ttc ttc acc gta ttg ttc gca atc	1267
Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile	
375 380 385	
ggt cgt ctg cca gga tgg atc gct cac tac cgc gag cag ctc ggt gca	1315
Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala	
390 395 400 405	
gca ggc aac aag atc aac cgc cca cgc cag gtc tac acc ggc aac gaa	1363
Ala Gly Asn Lys Ile Asn Arg Pro Arg Gln Val Tyr Thr Gly Asn Glu	
410 415 420	
tcc cgc aag ttg gtt cct cgc gag gag cgc taaatttagc ggatgattct	1413
Ser Arg Lys Leu Val Pro Arg Glu Glu Arg	
425 430	
cgt	1416

<210> 546  
 <211> 431  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 546  
 Val Ala Thr Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu  
 1 5 10 15  
 Phe Glu Met Asp Ile Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val  
 20 25 30  
 Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly  
 35 40 45  
 Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly  
 50 55 60  
 Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala  
 65 70 75 80  
 Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu  
 85 90 95  
 Leu Pro Thr Pro Asp Glu Leu His Lys Phe Asn Asp Glu Ile Arg His  
 100 105 110  
 His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro  
 115 120 125  
 Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu  
 130 135 140  
 Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu  
 145 150 155 160  
 Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala  
 165 170 175  
 Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn  
 180 185 190  
 Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro  
 195 200 205  
 Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys  
 210 215 220  
 Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr  
 225 230 235 240  
 Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala  
 245 250 255  
 Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln  
 260 265 270  
 Ala Val Leu Glu Met Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp  
 275 280 285

Ala Thr Glu Phe Met Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg  
290 295 300

Leu Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala  
305 310 315 320

Ala Ile Val Lys Glu Thr Ala His Glu Ile Leu Glu His Leu Gly Gly  
325 330 335

Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala  
340 345 350

Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr  
355 360 365

Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr  
370 375 380

Val Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg  
385 390 395 400

Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile Asn Arg Pro Arg Gln Val  
405 410 415

Tyr Thr Gly Asn Glu Ser Arg Lys Leu Val Pro Arg Glu Glu Arg  
420 425 430

<210> 547

<211> 942

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(919)

<223> RXA02621

<400> 547

atgtaccta ctggtgcgcg acacttcgct cactaaagtt,tttaaagatt tcgcttgaag 60

gcagaccata aggtctgcct ttctgcgtat taatgagtac atg tct gaa ctt att 115  
Met Ser Glu Leu Ile  
1 5

tgt gga cca gct att ctc ttc gca cca gct gga cgt gct gag atc att 163  
Cys Gly Pro Ala Ile Leu Phe Ala Pro Ala Gly Arg Ala Glu Ile Ile  
10 15 20

cca aaa gca gca tcg aag gcc gat atg gtc atc att gat ttg gaa gat 211  
Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile Ile Asp Leu Glu Asp  
25 30 35

ggg gca ggg gag gta gac cgt gag gtc gcc tac agg aac att aga gaa 259  
Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr Arg Asn Ile Arg Glu  
40 45 50

tcg ggg ttg gat cct aaa cga acc att gtg aga acc gta ggg ccg agc 307  
Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg Thr Val Gly Pro Ser  
55 60 65

gat cca cac ttt ttg gct gac gtg gag atg gtg aag tcc acg gat ttc 355  
 Asp Pro His Phe Leu Ala Asp Val Glu Met Val Lys Ser Thr Asp Phe  
 70 75 80 85  
 aca ctt gtt atg gtt cct aaa ctt ctt ggc agc gtg cct gag gaa tta 403  
 Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser Val Pro Glu Glu Leu  
 90 95 100  
 gat ggc ctc aac att atc gcc atg att gaa acc cct cag gct gca acc 451  
 Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr Pro Gln Ala Ala Thr  
 105 110 115  
 agc att cct cag att gct gcg gac cct aaa gtc gtt gga atg ttc tgg 499  
 Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val Val Gly Met Phe Trp  
 120 125 130  
 ggc gcg gag gat ctc aca cac ctc ttg gga ggc act cat tct agg ttc 547  
 Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly Thr His Ser Arg Phe  
 135 140 145  
 ttg ggt gat gag tcc aat gaa ggc tcc tac cga gac acc atg agg ctt 595  
 Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg Asp Thr Met Arg Leu  
 150 155 160 165  
 aca cgc gcc ctg atg cac ctc cac gcg gcg gcg aat ggg aag ttc acc 643  
 Thr Arg Ala Leu Met His Leu His Ala Ala Asn Gly Lys Phe Thr  
 170 175 180  
 att gat gcc atc cat gcg gat ttc cac gat gaa gag ggc ctc tat tta 691  
 Ile Asp Ala Ile His Ala Asp Phe His Asp Glu Glu Gly Leu Tyr Leu  
 185 190 195  
 gaa gcg gtc gat gct gcg cgg act ggt ttc gct ggc acc gca tgc att 739  
 Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala Gly Thr Ala Cys Ile  
 200 205 210  
 cac ccc aag cag atc gag att gtt cgg aga gcc tat cgg cca gag gct 787  
 His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala Tyr Arg Pro Glu Ala  
 215 220 225  
 aac cag ttg gag tgg gcg aag aaa gtg gtg gag gaa gca gaa aac cat 835  
 Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu Glu Ala Glu Asn His  
 230 235 240 245  
 cca ggt gcg ttc aaa ctg gat ggt cag atg att gat gct ccg ttg att 883  
 Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile Asp Ala Pro Leu Ile  
 250 255 260  
 tcg cag gcg cgg atg gtt att tcg cgt cag cct gct tgattagttc 929  
 Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro Ala  
 265 270  
 aagcgttttt tcg 942

&lt;210&gt; 548

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 548

Met Ser Glu Leu Ile Cys Gly Pro Ala Ile Leu Phe Ala Pro Ala Gly  
 1 5 10 15

Arg Ala Glu Ile Ile Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile  
 20 25 30

Ile Asp Leu Glu Asp Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr  
 35 40 45

Arg Asn Ile Arg Glu Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg  
 50 55 60

Thr Val Gly Pro Ser Asp Pro His Phe Leu Ala Asp Val Glu Met Val  
 65 70 75 80

Lys Ser Thr Asp Phe Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser  
 85 90 95

Val Pro Glu Glu Leu Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr  
 100 105 110

Pro Gln Ala Ala Thr Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val  
 115 120 125

Val Gly Met Phe Trp Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly  
 130 135 140

Thr His Ser Arg Phe Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg  
 145 150 155 160

Asp Thr Met Arg Leu Thr Arg Ala Leu Met His Leu His Ala Ala Ala  
 165 170 175

Asn Gly Lys Phe Thr Ile Asp Ala Ile His Ala Asp Phe His Asp Glu  
 180 185 190

Glu Gly Leu Tyr Leu Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala  
 195 200 205

Gly Thr Ala Cys Ile His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala  
 210 215 220

Tyr Arg Pro Glu Ala Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu  
 225 230 235 240

Glu Ala Glu Asn His Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile  
 245 250 255

Asp Ala Pro Leu Ile Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro  
 260 265 270

Ala

&lt;210&gt; 549

&lt;211&gt; 2337

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2314)

&lt;223&gt; RXN00519

&lt;400&gt; 549

```

tttccatgcg gggctgaaac tgccaccata ggcgccagca attagtagaa cactgtattc 60

taggtagctg aacaaaagag cccatcaacc aaggagactc atg gct aag atc atc 115
                                         Met Ala Lys Ile Ile
                                         1 5

tgg acc cgc acc gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag 163
Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys
          10          15          20

ccg gtc gtc gag gca ttt gct gct acc gcg ggc att gag gtc gag acc 211
Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr
          25          30          35

cgg gac att tca ctc gct gga cgc atc ctc gcc cag ttc cca gag cgc 259
Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala Gln Phe Pro Glu Arg
          40          45          50

ctc acc gaa gat cag aag gta ggc aac gca ctc gca gaa ctc ggc gag 307
Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu Ala Glu Leu Gly Glu
          55          60          65

ctt gct aag act cct gaa gca aac atc att aag ctt cca aac atc tcc 355
Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser
          70          75          80          85

gct tct gtt cca cag ctc aag gct gct att aag gaa ctg cag gac cag 403
Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys Glu Leu Gln Asp Gln
          90          95          100

ggc tac gac atc cca gaa ctg cct gat aac gcc acc acc gac gag gaa 451
Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala Thr Thr Asp Glu Glu
          105          110          115

aaa gac atc ctc gca cgc tac aac gct gtt aag ggt tcc gct gtg aac 499
Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys Gly Ser Ala Val Asn
          120          125          130

cca gtg ctg cgt gaa ggc aac tct gac cgc cgc gca cca atc gct gtc 547
Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro Ile Ala Val
          135          140          145

aag aac ttt gtt aag aag ttc cca cac cgc atg ggc gag tgg tct gca 595
Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala
          150          155          160          165

gat tcc aag acc aac gtt gca acc atg gat gca aac gac ttc cgc cac 643
Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala Asn Asp Phe Arg His
          170          175          180

aac gag aag tcc atc atc ctc gac gct gct gat gaa gtt cag atc aag 691
Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp Glu Val Gln Ile Lys
          185          190          195

cac atc gca gct gac ggc acc gag acc atc ctc aag gac agc ctc aag 739

```



His	Ile	Ala	Ala	Asp	Gly	Thr	Glu	Thr	Ile	Leu	Lys	Asp	Ser	Leu	Lys		
		200					205					210					
ctt	ctt	gaa	ggc	gaa	gtt	cta	gac	gga	acc	gtt	ctg	tcc	gca	aag	gca	787	
Leu	Leu	Glu	Gly	Glu	Val	Leu	Asp	Gly	Thr	Val	Leu	Ser	Ala	Lys	Ala		
		215				220					225						
ctg	gac	gca	ttc	ctt	ctc	gag	cag	gtc	gct	cgc	gca	aag	gca	gaa	ggt	835	
Leu	Asp	Ala	Phe	Leu	Leu	Glu	Gln	Val	Ala	Arg	Ala	Lys	Ala	Glu	Gly		
		230			235					240					245		
atc	ctc	ttc	tcc	gca	cac	ctg	aag	gcc	acc	atg	atg	aag	gtc	tcc	gac	883	
Ile	Leu	Phe	Ser	Ala	His	Leu	Lys	Ala	Thr	Met	Met	Lys	Val	Ser	Asp		
				250					255					260			
cca	atc	atc	ttc	ggc	cac	gtt	gtg	cgc	gct	tac	ttc	gca	gac	gtt	ttc	931	
Pro	Ile	Ile	Phe	Gly	His	Val	Val	Arg	Ala	Tyr	Phe	Ala	Asp	Val	Phe		
			265					270					275				
gca	cag	tac	ggt	gag	cag	ctg	ctc	gca	gct	ggc	ctc	aac	ggc	gaa	aac	979	
Ala	Gln	Tyr	Gly	Glu	Gln	Leu	Leu	Ala	Ala	Gly	Leu	Asn	Gly	Glu	Asn		
		280					285					290					
ggc	ctc	gct	gca	atc	ctc	tcc	ggc	ttg	gag	tcc	ctg	gac	aac	ggc	gaa	1027	
Gly	Leu	Ala	Ala	Ile	Leu	Ser	Gly	Leu	Glu	Ser	Leu	Asp	Asn	Gly	Glu		
		295				300					305						
gaa	atc	aag	gct	gca	ttc	gag	aag	ggc	ttg	gaa	gac	ggc	cca	gac	ctg	1075	
Glu	Ile	Lys	Ala	Ala	Phe	Glu	Lys	Gly	Leu	Glu	Asp	Gly	Pro	Asp	Leu		
					315					320					325		
gcc	atg	gtt	aac	tcc	gct	cgc	ggc	atc	acc	aac	ctg	cat	gtc	cct	tcc	1123	
Ala	Met	Val	Asn	Ser	Ala	Arg	Gly	Ile	Thr	Asn	Leu	His	Val	Pro	Ser		
				330					335					340			
gat	gtc	atc	gtg	gac	gct	tcc	atg	cca	gca	atg	att	cgt	acc	tcc	ggc	1171	
Asp	Val	Ile	Val	Asp	Ala	Ser	Met	Pro	Ala	Met	Ile	Arg	Thr	Ser	Gly		
			345					350					355				
cac	atg	tgg	aac	aaa	gac	gac	cag	gag	cag	gac	acc	ctg	gca	atc	atc	1219	
His	Met	Trp	Asn	Lys	Asp	Asp	Gln	Glu	Gln	Asp	Thr	Leu	Ala	Ile	Ile		
		360					365					370					
cca	gac	tcc	tcc	tac	gct	ggc	gtc	tac	cag	acc	gtt	atc	gaa	gac	tgc	1267	
Pro	Asp	Ser	Ser	Tyr	Ala	Gly	Val	Tyr	Gln	Thr	Val	Ile	Glu	Asp	Cys		
		375				380					385						
cgc	aag	aac	ggc	gca	ttc	gat	cca	acc	acc	atg	ggt	acc	gtc	cct	aac	1315	
Arg	Lys	Asn	Gly	Ala	Phe	Asp	Pro	Thr	Thr	Met	Gly	Thr	Val	Pro	Asn		
					395					400					405		
gtt	ggt	ctg	atg	gct	cag	aag	gct	gaa	gag	tac	ggc	tcc	cat	gac	aag	1363	
Val	Gly	Leu	Met	Ala	Gln	Lys	Ala	Glu	Glu	Tyr	Gly	Ser	His	Asp	Lys		
				410					415					420			
acc	ttc	cgc	atc	gaa	gca	gac	ggt	gtg	gtt	cag	gtt	gtt	tcc	tcc	aac	1411	
Thr	Phe	Arg	Ile	Glu	Ala	Asp	Gly	Val	Val	Gln	Val	Val	Ser	Ser	Asn		
			425					430					435				
ggc	gac	gtt	ctc	atc	gag	cac	gac	gtt	gag	gca	aac	gac	atc	tgg	cgt	1459	
Gly	Asp	Val	Leu	Ile	Glu	His	Asp	Val	Glu	Ala	Asn	Asp	Ile	Trp	Arg		

440	445	450	
gca tgc cag gtc aag gat gcc cca atc cag gat tgg gta aag ctt gct Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala 455 460 465			1507
gtc acc cgc tcc cgt ctc tcc gga atg cct gca gtg ttc tgg ttg gat Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp 470 475 480 485			1555
cca gag cgc gca cac gac cgc aac ctg gct tcc ctc gtt gag aag tac Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr 490 495 500			1603
ctg gct gac cac gac acc gag ggc ctg gac atc cag atc ctc tcc cct Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro 505 510 515			1651
gtt gag gca acc cag ctc tcc atc gac cgc atc cgc cgt ggc gag gac Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp 520 525 530			1699
acc atc tct gtc acc ggt aac gtt ctg cgt gac tac aac acc gac ctc Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu 535 540 545			1747
ttc cca atc ctg gag ctg ggc acc tct gca aag atg ctg tct gtc gtt Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val 550 555 560 565			1795
cct ttg atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser 570 575 580			1843
gct cct aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp 585 590 595			1891
gat tcc ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu 600 605 610			1939
ctc aac aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu 615 620 625			1987
gac aag gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg 630 635 640 645			2035
aag gtt ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys 650 655 660			2083
ttc tgg gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala 665 670 675			2131
gct acc ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp 680 685 690			2179

atc gat gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt 2227  
 Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly  
 695 700 705

ggc tac tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca 2275  
 Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro  
 710 715 720 725

gtc gca cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct 2324  
 Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys  
 730 735

tcacaaaaag cgc 2337

<210> 550

<211> 738

<212> PRT

<213> Corynebacterium glutamicum

<400> 550

Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala  
 1 5 10 15

Thr Tyr Ser Leu Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly  
 20 25 30

Ile Glu Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala  
 35 40 45

Gln Phe Pro Glu Arg Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu  
 50 55 60

Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys  
 65 70 75 80

Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys  
 85 90 95

Glu Leu Gln Asp Gln Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala  
 100 105 110

Thr Thr Asp Glu Glu Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys  
 115 120 125

Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg  
 130 135 140

Ala Pro Ile Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met  
 145 150 155 160

Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala  
 165 170 175

Asn Asp Phe Arg His Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp  
 180 185 190

Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu  
 195 200 205

Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val  
 210 215 220  
 Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg  
 225 230 235 240  
 Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met  
 245 250 255  
 Met Lys Val Ser Asp Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr  
 260 265 270  
 Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly  
 275 280 285  
 Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser  
 290 295 300  
 Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu  
 305 310 315 320  
 Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn  
 325 330 335  
 Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met  
 340 345 350  
 Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp  
 355 360 365  
 Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr  
 370 375 380  
 Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met  
 385 390 395 400  
 Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr  
 405 410 415  
 Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln  
 420 425 430  
 Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Ala  
 435 440 445  
 Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp  
 450 455 460  
 Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala  
 465 470 475 480  
 Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser  
 485 490 495  
 Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile  
 500 505 510  
 Gln Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile  
 515 520 525  
 Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp

530	535	540
Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys 545 550 555 560		
Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr 565 570 575		
Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Gln Glu Glu 580 585 590		
Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu 595 600 605		
Ser Phe Arg His Glu Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val 610 615 620		
Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu 625 630 635 640		
Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His 645 650 655		
Phe Trp Leu Thr Lys Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu 660 665 670		
Asp Ala Asp Leu Ala Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn 675 680 685		
Thr Gly Ala Ala Asp Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly 690 695 700		
Ala Thr Asp Leu Gly Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr 705 710 715 720		
Asn Ile Met Arg Pro Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu 725 730 735		

Lys Lys

<210> 551  
 <211> 1059  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1059)  
 <223> FRXA00521

<400> 551	
ctc gac gct gct gat gaa gtt cag atc aag cac atc gca gct gac ggc 48	
Leu Asp Ala Ala Asp Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly	
1 5 10 15	
acc gag acc atc ctc aag gac agc ctc aag ctt ctt gaa ggc gaa gtt 96	
Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val	
20 25 30	

cta gac gga acc gtt ctg tcc gca aag gca ctg gac gca ttc ctt ctc	144
Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu	
35 40 45	
gag cag gtc gct cgc gca aag gca gaa ggt atc ctc ttc tcc gca cac	192
Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His	
50 55 60	
ctg aag gcc acc atg atg aag gtc tcc gac cca atc atc ttc ggc cac	240
Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His	
65 70 75 80	
gtt gtg cgc gct tac ttc gca gac gtt ttc gca cag tac ggt gag cag	288
Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln	
85 90 95	
ctg ctc gca gct ggc ctc aac ggc gaa aac ggc ctc gct gca atc ctc	336
Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu	
100 105 110	
tcc ggc ttg gag tcc ctg gac aac ggc gaa gaa atc aag gct gca ttc	384
Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe	
115 120 125	
gag aag ggc ttg gaa gac ggc cca gac ctg gcc atg gtt aac tcc gct	432
Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala	
130 135 140	
cgc ggc atc acc aac ctg cat gtc cct tcc gat gtc atc gtg gac gct	480
Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala	
145 150 155 160	
tcc atg cca gca atg att cgt acc tcc ggc cac atg tgg aac aaa gac	528
Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp	
165 170 175	
gac cag gag cag gac acc ctg gca atc atc cca gac tcc tcc tac gct	576
Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala	
180 185 190	
ggc gtc tac cag acc gtt atc gaa gac tgc cgc aag aac ggc gca ttc	624
Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe	
195 200 205	
gat cca acc acc atg ggt acc gtc cct aac gtt ggt ctg atg gct cag	672
Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln	
210 215 220	
aag gct gaa gag tac ggc tcc cat gac aag acc ttc cgc atc gaa gca	720
Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala	
225 230 235 240	
gac ggt gtg gtt cag gtt gtt tcc tcc aac ggc gac gtt ctc atc gag	768
Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu	
245 250 255	
cac gac gtt gag gca aat gac atc tgg cgt gca tgc cag gtc aag gat	816
His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp	
260 265 270	
gcc cca atc cag gat tgg gta aag ctt gct gtc acc cgc tcc cgt ctc	864

Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu  
 275 280 285

tcc gga atg cct gca gtg ttc tgg ttg gat cca gag cgc gca cac gac 912  
 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp  
 290 295 300

cgc aac ctg gct tcc ctc gtt gag aag tac ctg gct gac cac gac acc 960  
 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr  
 305 310 315 320

gag ggc ctg gac atc cag atc ctc tac cct gtt gag gca acc cag ctc 1008  
 Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu  
 325 330 335

tcc atc gac cgc atc cgc cgt ggc gag gac acc atc tct gtc acc ggt 1056  
 Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly  
 340 345 350

aac 1059  
 Asn

<210> 552  
 <211> 353  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 552  
 Leu Asp Ala Ala Asp Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly  
 1 5 10 15  
 Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val  
 20 25 30  
 Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu  
 35 40 45  
 Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His  
 50 55 60  
 Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His  
 65 70 75 80  
 Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln  
 85 90 95  
 Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu  
 100 105 110  
 Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe  
 115 120 125  
 Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala  
 130 135 140  
 Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala  
 145 150 155 160  
 Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp

165                      170                      175  
 Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala  
                          180                      185                      190  
 Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe  
                          195                      200                      205  
 Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln  
                          210                      215                      220  
 Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala  
                          225                      230                      235                      240  
 Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu  
                          245                      250                      255  
 His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp  
                          260                      265                      270  
 Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu  
                          275                      280                      285  
 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp  
                          290                      295                      300  
 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr  
                          305                      310                      315                      320  
 Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu  
                          325                      330                      335  
 Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly  
                          340                      345                      350

Asn

<210> 553  
 <211> 1694  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1671)  
 <223> RXN02209

<400> 553  
 acc gag tcc acc gtt gtt cct tcc atc gct ggc cct aag cgc cca cag    48  
 Thr Glu Ser Thr Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln  
       1                      5                      10                      15  
 gac cgc atc ctt ctc tcc gag gca aag gag cag ttc cgt aag gat ctg    96  
 Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu  
                          20                      25                      30  
 cca acc tac acc gac gac gct gtt tcc gta gac acc tcc atc cct gca    144  
 Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala  
                          35                      40                      45



acc cgc atg gtt aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa	192
Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu	
50 55 60	
gct gac aac tac aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct	240
Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala	
65 70 75 80	
act ggc gca gaa gga cgt cct tcc aag cca gtc acc gtt gca tcc cca	288
Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro	
85 90 95	
cag ggt ggc gag tac acc atc gac cac ggc atg gtt gca att gca tcc	336
Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser	
100 105 110	
atc acc tct tgc acc aac acc tct aac cca tcc gtg atg atc ggc gct	384
Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala	
115 120 125	
ggc ctg atc gca cgt aag gca gca gaa aag ggc ctc aag tcc aag cct	432
Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro	
130 135 140	
tgg gtt aag acc atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac	480
Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr	
145 150 155 160	
tac cag cgc gca gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac	528
Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr	
165 170 175	
ctc tcc ggc ttc ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg	576
Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu	
180 185 190	
cca gag gaa atc tcc gct gcg atc aac gag cac gac ctg acc gca acc	624
Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr	
195 200 205	
gca gtt ttg tcc ggt aac cgt aac ttc gag gga cgt atc tcc cct gac	672
Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp	
210 215 220	
gtt aag atg aac tac ctg gca tcc cca atc atg gtc att gct tac gca	720
Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala	
225 230 235 240	
atc gct ggc acc atg gac ttc gac ttc gag aac gaa gct ctt gga cag	768
Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln	
245 250 255	
gac cag gac ggc aac gac gtc ttc ctg aag gac atc tgg cct tcc acc	816
Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr	
260 265 270	
gag gaa atc gaa gac acc atc cag cag gca atc tcc cgt gag ctt tac	864
Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr	
275 280 285	

gaa gct gac tac gca gat gtc ttc aag ggt gac aag cag tgg cag gaa	912
Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu	
290 295 300	
ctc gat gtt cct acc ggt gac acc ttc gag tgg gac gag aac tcc acc	960
Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr	
305 310 315 320	
tac atc cgc aag gca cct tac ttc gac ggc atg cct gtc gag cca gtg	1008
Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val	
325 330 335	
gca gtc acc gac atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac	1056
Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp	
340 345 350	
tct gtc acc acc gac cac atc tcc cct gct tcc tcc att aag cca ggt	1104
Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly	
355 360 365	
acc cct gca gct cag tac ttg gat gag cac ggt gtg gaa cgc cac gac	1152
Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp	
370 375 380	
tac aac tcc ctg ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc	1200
Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg	
385 390 395 400	
ggc acc ttc gcc aac atc cgc ctc cag aac cag ctg gtt gac atc gca	1248
Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala	
405 410 415	
ggt ggc tac acc cgc gac ttc acc cag gag ggt gct cca cag gcg ttc	1296
Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe	
420 425 430	
atc tac gac gct tcc gtc aac tac aag gct gct ggc att ccg ctg gtc	1344
Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val	
435 440 445	
gtc ttg ggc ggc aag gag tac ggc acc ggt tct tcc cgt gac tgg gca	1392
Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala	
450 455 460	
gct aag ggc act aac ctg ctc gga att cgc gca gtt atc acc gag tcc	1440
Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser	
465 470 475 480	
ttc gag cgt att cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca	1488
Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro	
485 490 495	
ctg cag ttc cct gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc	1536
Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly	
500 505 510	
acc gag acc ttc gac atc acc gga ctg acc gca ctt aac gag ggc gag	1584
Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu	
515 520 525	
act cct aag act gtc aag gtc acc gca acc aag gag aac ggc gac gtc	1632

Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val  
 530 535 540  
 gtc gag ttc gac gca att tgt ccg cat cga cac ccc agg tgaggctgac 1681  
 Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg  
 545 550 555

tactaccgcc acg 1694

<210> 554

<211> 557

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Thr Glu Ser Thr Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln  
 1 5 10 15

Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu  
 20 25 30

Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala  
 35 40 45

Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu  
 50 55 60

Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala  
 65 70 75 80

Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro  
 85 90 95

Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser  
 100 105 110

Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala  
 115 120 125

Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro  
 130 135 140

Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr  
 145 150 155 160

Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr  
 165 170 175

Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu  
 180 185 190

Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr  
 195 200 205

Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp  
 210 215 220

Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala  
 225 230 235 240

790

<210> 555  
 <211> 1682  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1659)  
 <223> FRXA02209

<400> 555

```

gtt gtt cct tcc atc gct ggc cct aag cgc cca cag gac cgc atc ctt   48
Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu
  1                               10                          15

ctc tcc gag gca aag gag cag ttc cgt aag gat ctg cca acc tac acc   96
Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
                20                      25                      30

gac gac gct gtt tcc gta gac acc tcc atc cct gca acc cgc atg gtt   144
Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
                35                      40                      45

aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa gct gac aac tac   192
Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
                50                      55                      60

aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct act ggc gca gaa   240
Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
                65                      70                      75                      80

gga cgt cct tcc aag cca gtc acc gtt gca tcc cca cag ggt ggc gag   288
Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
                85                      90                      95

tac acc atc gac cac ggc atg gtt gca att gca tcc atc acc tct tgc   336
Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
                100                      105                      110

acc aac acc tct aac cca tcc gtg atg atc ggc gct ggc ctg atc gca   384
Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
                115                      120                      125

cgt aag gca gca gaa aag ggc ctc aag tcc aag cct tgg gtt aag acc   432
Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
                130                      135                      140

atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac tac cag cgc gca   480
Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
                145                      150                      155                      160

gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac ctc tcc ggc ttc   528
Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
                165                      170                      175

ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg cca gag gaa atc   576
Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile
                180                      185                      190

tcc gct gcg atc aac gag cac gac ctg acc gca acc gca gtt ttg tcc   624
Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser

```

195	200	205	
ggt aac cgt aac ttc gag gga cgt atc tcc cct gac gtt aag atg aac Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn 210 215 220			672
tac ctg gca tcc cca atc atg gtc att gct tac gca atc gct ggc acc Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr 225 230 235 240			720
atg gac ttc gac ttc gag aac gaa gct ctt gga cag gac cag gac ggc Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly 245 250 255			768
aac gac gtc ttc ctg aag gac atc tgg cct tcc acc gag gaa atc gaa Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu 260 265 270			816
gac acc atc cag cag gca atc tcc cgt gag ctt tac gaa gct gac tac Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr 275 280 285			864
gca gat gtc ttc aag ggt gac aag cag tgg cag gaa ctc gat gtt cct Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro 290 295 300			912
acc ggt gac acc ttc gag tgg gac gag aac tcc acc tac atc cgc aag Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys 305 310 315 320			960
gca cct tac ttc gac ggc atg cct gtc gag cca gtg gca gtc acc gac Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp 325 330 335			1008
atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac tct gtc acc acc Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr 340 345 350			1056
gac cac atc tcc cct gct tcc tcc att aag cca ggt acc cct gca gct Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala 355 360 365			1104
cag tac ttg gat gag cac ggt gtg gaa cgc cac gac tac aac tcc ctg Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu 370 375 380			1152
ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc ggc acc ttc gcc Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala 385 390 395 400			1200
aac atc cgc ctc cag aac cag ctg gtt gac atc gca ggt ggc tac acc Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr 405 410 415			1248
cgc gac ttc acc cag gag ggt gct cca cag gcg ttc atc tac gac gct Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala 420 425 430			1296
tcc gtc aac tac aag gct gct ggc att ccg ctg gtc gtc ttg ggc ggc Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly 435 440 445			1344

aag gag tac ggc acc ggt tct tcc cgt gac tgg gca gct aag ggc act 1392  
 Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr  
 450 455 460

aac ctg ctc gga att cgc gca gtt atc acc gag tcc ttc gag cgt att 1440  
 Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile  
 465 470 475 480

cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca ctg cag ttc cct 1488  
 His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro  
 485 490 495

gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc acc gag acc ttc 1536  
 Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe  
 500 505 510

gac atc acc gga ctg acc gca ctt aac gag ggc gag act cct aag act 1584  
 Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr  
 515 520 525

gtc aag gtc acc gca acc aag gag aac ggc gac gtc gtc gag ttc gac 1632  
 Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp  
 530 535 540

gca att tgt ccg cat cga cac ccc agg tgaggctgac tactaccgcc 1679  
 Ala Ile Cys Pro His Arg His Pro Arg  
 545 550

acg 1682

<210> 556

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 556

Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu  
 1 5 10 15

Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr  
 20 25 30

Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val  
 35 40 45

Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr  
 50 55 60

Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu  
 65 70 75 80

Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu  
 85 90 95

Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys  
 100 105 110

Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala  
 115 120 125

Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr  
 130 135 140  
 Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala  
 145 150 155 160  
 Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe  
 165 170 175  
 Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile  
 180 185 190  
 Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser  
 195 200 205  
 Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn  
 210 215 220  
 Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr  
 225 230 235 240  
 Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly  
 245 250 255  
 Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu  
 260 265 270  
 Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr  
 275 280 285  
 Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro  
 290 295 300  
 Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys  
 305 310 315 320  
 Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp  
 325 330 335  
 Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr  
 340 345 350  
 Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala  
 355 360 365  
 Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu  
 370 375 380  
 Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala  
 385 390 395 400  
 Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr  
 405 410 415  
 Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala  
 420 425 430  
 Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly  
 435 440 445



Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr  
 450 455 460  
 Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile  
 465 470 475 480  
 His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro  
 485 490 495  
 Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe  
 500 505 510  
 Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr  
 515 520 525  
 Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp  
 530 535 540  
 Ala Ile Cys Pro His Arg His Pro Arg  
 545 550

<210> 557  
 <211> 874  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(874)  
 <223> RXN02213

<400> 557  
 ttctgtgga tgagaatccg atgtttttct cagcccggt cagccgaagc agacgccgtc 60  
 gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag 115  
 Val Thr Glu Ser Lys 5  
 1  
 aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat 163  
 Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr 20  
 10 15  
 gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac 211  
 Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr 35  
 25 30  
 tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca 259  
 Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala 50  
 40 45  
 aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307  
 Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser 65  
 55 60  
 tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355  
 Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met 85  
 70 75 80  
 cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt 403  
 Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg

90	95	100	
gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg			451
Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu			
105	110	115	
aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc			499
Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe			
120	125	130	
ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc			547
Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg			
135	140	145	
aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc			595
Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser			
150	155	160	165
aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac			643
Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn			
170	175	180	
att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac			691
Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr			
185	190	195	
cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc			739
Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly			
200	205	210	
ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca			787
Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala			
215	220	225	
atg ctc ggc cag cca gtg tcc atg ctg atc cct cgc gtt gtt ggc ttc			835
Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro Arg Val Val Gly Phe			
230	235	240	245
aag ttg acc ggc gag atc cca gta ggc gtt acc gca act			874
Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr Ala Thr			
250	255		

&lt;210&gt; 558

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 558

Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val		
1	5	10
15		

Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met		
20	25	30

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg		
35	40	45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala		
50	55	60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro  
 65 70 75 80  
 Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp  
 85 90 95  
 Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn  
 100 105 110  
 Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val  
 115 120 125  
 Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu  
 130 135 140  
 Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly  
 145 150 155 160  
 Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile  
 165 170 175  
 Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn  
 180 185 190  
 Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr  
 195 200 205  
 Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile  
 210 215 220  
 Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro  
 225 230 235 240  
 Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr  
 245 250 255

Ala Thr

<210> 559  
 <211> 817  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(817)  
 <223> FRXA02213

<400> 559  
 ttctgtggaa tgagaatccg atgtttttct cagccggct cagccgaagc agacgccgtc 60  
 gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag 115  
 Val Thr Glu Ser Lys  
 1 5  
 aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat 163  
 Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr  
 10 15 20

gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac 211  
 Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr  
                   25                                  30                                  35

tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca 259  
 Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala  
                   40                                  45                                  50

aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307  
 Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser  
                   55                                  60                                  65

tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355  
 Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met  
                   70                                  75                                  80                                  85

cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt 403  
 Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg  
                   90                                  95                                  100

gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg 451  
 Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu  
                   105                                  110                                  115

aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc 499  
 Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe  
                   120                                  125                                  130

ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc 547  
 Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg  
                   135                                  140                                  145

aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc 595  
 Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser  
                   150                                  155                                  160                                  165

aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac 643  
 Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn  
                   170                                  175                                  180

att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac 691  
 Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr  
                   185                                  190                                  195

cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc 739  
 Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly  
                   200                                  205                                  210

ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca 787  
 Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala  
                   215                                  220                                  225

atg ctc ggc cag cca gtg tcc atg ctg atc 817  
 Met Leu Gly Gln Pro Val Ser Met Leu Ile  
                   230                                  235

&lt;210&gt; 560

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 560

Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val  
 1 5 10 15

Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met  
 20 25 30

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg  
 35 40 45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala  
 50 55 60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro  
 65 70 75 80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp  
 85 90 95

Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn  
 100 105 110

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val  
 115 120 125

Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu  
 130 135 140

Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly  
 145 150 155 160

Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile  
 165 170 175

Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn  
 180 185 190

Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr  
 195 200 205

Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile  
 210 215 220

Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile  
 225 230 235

&lt;210&gt; 561

&lt;211&gt; 2891

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2868)

&lt;223&gt; RXA02056

&lt;400&gt; 561

cgc cac tct gtt cca cgt cta acc aag ggc cag ggc acc atc atc ggt 48  
 Arg His Ser Val Pro Arg Leu Thr Lys Gly Gln Gly Thr Ile Ile Gly

1	5	10	15	
gtc ggt tcc atg gat tac cca gca gag ttc cag ggc gct tca gaa gac	96			
Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp				
20	25	30		
cgc ctt gca gag ctc ggc gtt ggc aaa ctt gtc acc atc acc tcc acc	144			
Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr				
35	40	45		
tac gat cac cgc gtg atc cag ggt gct gtg tcc ggt gaa ttc ctg cgc	192			
Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg				
50	55	60		
acc atg tct cgc ctg ctc acc gat gat tcc ttc tgg gat gag atc ttc	240			
Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe				
65	70	75	80	
gac gca atg aac gtt cct tac acc cca atg cgt tgg gca cag gac gtt	288			
Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val				
85	90	95		
cca aac acc ggt gtt gat aag aac acc cgc gtc atg cag ctc att gag	336			
Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu				
100	105	110		
gca tac cgc tcc cgt gga cac ctc atc gct gac acc aac cca ctt tca	384			
Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser				
115	120	125		
tgg gtt cag cct ggc atg cca gtt cca gac cac cgc gac ctc gac atc	432			
Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile				
130	135	140		
gag acc cac aac ctg acc atc tgg gat ctg gac cgt acc ttc aac gtc	480			
Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val				
145	150	155	160	
ggt ggc ttc ggc ggc aag gag acc atg acc ctg cgc gag gta ctg tcc	528			
Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser				
165	170	175		
cgc ctc cgc gct gcg tac acc ctc aag gtc ggc tcc gaa tac acc cac	576			
Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His				
180	185	190		
atc ctg gac cgc gac gag cgc acc tgg ctg cag gac cgc ctc gag gcc	624			
Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala				
195	200	205		
gga atg cca aag cca acc cag gca gag cag aag tac atc ctg cag aag	672			
Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys				
210	215	220		
ctg aac gcc gcg gag gct ttc gag aac ttc ctg cag acc aag tac gtc	720			
Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val				
225	230	235	240	
ggc cag aag cgc ttc tcc ctc gaa ggt gca gaa gca ctt atc cca ctg	768			
Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu				
245	250	255		

atg gac tcc gcc atc gac acc gcc gca ggc caa ggc ctc gac gaa gtt	816
Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val	
260 265 270	
gtc atc ggt atg cca cac cgt ggt cgc ctc aac gtg ctg ttc aac atc	864
Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile	
275 280 285	
gtg ggc aag cca ctg gca tcc atc ttc aac gag ttt gaa ggc caa atg	912
Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met	
290 295 300	
gag cag ggc cag atc ggt ggc tcc ggt gac gtg aag tac cac ctc ggt	960
Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly	
305 310 315 320	
tcc gaa ggc cag cac ctg cag atg ttc ggc gac ggc gag atc aag gtc	1008
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val	
325 330 335	
tcc ctg act gct aac ccg tcc cac ctg gaa gct gtt aac cca gcg atg	1056
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met	
340 345 350	
gaa ggt att gtc cgc gca aag cag gac tac ctg gac aag ggc gta gac	1104
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp	
355 360 365	
ggc aag act gtt gtg cca ctg ctg ctc cac ggt gac gct gca ttc gca	1152
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala	
370 375 380	
ggc ctg ggc atc gtg cca gaa acc atc aac ctg gct aag ctg cgt ggc	1200
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly	
385 390 395 400	
tac gac gtc ggc ggc acc atc cac atc gtg gtg aac aac cag atc ggc	1248
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly	
405 410 415	
ttc acc acc acc cca gac tcc agc cgc tcc atg cac tac gca acc gac	1296
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp	
420 425 430	
tac gcc aag gca ttc ggc tgc cca gtc ttc cac gtc aac ggc gac gac	1344
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp	
435 440 445	
cca gag gca gtt gtc tgg gtt ggc cag ctg gcc acc gag tac cgt cgt	1392
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg	
450 455 460	
cgc ttc ggc aag gac gtc ttc atc gac ctc gtc tgc tac cgc ctc cgc	1440
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg	
465 470 475 480	
ggc cac aac gaa gct gat gat cct tcc atg acc cag cca aag atg tat	1488
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr	
485 490 495	

gag ctc atc acc ggc cgc gag acc gtt cgt gct cag tac acc gaa gac	1536
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp	
500 505 510	
ctg ctc gga cgt gga gac ctc tcc aac gaa gat gca gaa gca gtc gtc	1584
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	
515 520 525	
cgc gac ttc cac gac cag atg gaa tct gtg ttc aac gaa gtc aag gaa	1632
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu	
530 535 540	
ggc ggc aag aag cag gct gag gca cag acc ggc atc acc ggc tcc cag	1680
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln	
545 550 555 560	
aag ctt cca cac ggc ctt gag acc aac atc tcc cgt gaa gag ctc ctg	1728
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	
565 570 575	
gaa ctg gga cag gct ttc gcc aac acc cca gaa ggc ttc aac tac cac	1776
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His	
580 585 590	
cca cgt gtg gct ccc gtt gct aag aag cgc gtc tcc tct gtc acc gaa	1824
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu	
595 600 605	
ggt ggc atc gac tgg gca tgg ggc gag ctc ctc gcc ttc ggt tcc ctg	1872
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu	
610 615 620	
gct aac tcc ggc cgc ttg gtt cgc ctt gca ggt gaa gat tcc cgc cgc	1920
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg	
625 630 635 640	
ggt acc ttc acc cag cgc cac gca gtt gcc atc gac cca gcg acc gct	1968
Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala	
645 650 655	
gaa gag ttc aac cca ctc cac gag ctt gca cag tcc aag ggc aac aac	2016
Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn	
660 665 670	
ggt aag ttc ctg gtc tac aac tcc gca ctg acc gag tac gca ggc atg	2064
Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met	
675 680 685	
ggc ttc gag tac ggc tac tcc gta gga aac gaa gac tcc atc gtt gca	2112
Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala	
690 695 700	
tgg gaa gca cag ttc ggc gac ttc gcc aac ggc gct cag acc atc atc	2160
Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile	
705 710 715 720	
gat gag tac gtc tcc tca ggc gaa gct aag tgg ggc cag acc tcc aag	2208
Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys	
725 730 735	
ctg atc ctt ctg ctg cct cac ggc tac gaa ggc cag ggc cca gac cac	2256



Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His	
740 745 750	
tct tcc gca cgt atc gag cgc ttc ctg cag ctg tgc gct gag ggt tcc	2304
Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser	
755 760 765	
atg act gtt gct cag cca tcc acc cca gca aac cac ttc cac cta ctg	2352
Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu	
770 775 780	
cgt cgt cac gct ctg tcc gac ctg aag cgt cca ctg gtt atc ttc acc	2400
Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr	
785 790 795 800	
ccg aag tcc atg ctg cgt aac aag gct gct gcc tcc gca cca gaa gac	2448
Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp	
805 810 815	
ttc act gag gtc acc aag ttc cag tcc gtg atc aac gat cca aac gtt	2496
Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val	
820 825 830	
gca gat gca gcc aag gtg aag aag gtc atg ctg gtc tcc gcc aag ctg	2544
Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu	
835 840 845	
tac tac gaa ttg gca aag cgc aag gag aag gac gga cgc gac gac atc	2592
Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile	
850 855 860	
gcg atc gtt cgt atc gaa atg ctc cac cca att ccg ttc aac cgc atc	2640
Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile	
865 870 875 880	
tcc gag gct ctt gcc ggc tac cct aac gct gag gaa gtc ctc ttc gtt	2688
Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val	
885 890 895	
cag gat gag cca gca aac cag ggc cca tgg ccg ttc tac cag gag cac	2736
Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His	
900 905 910	
ctc cca gag ctg atc ccg aac atg cca aag atg cgc cgc gtt tcc cgc	2784
Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg	
915 920 925	
cgc gct cag tcc tcc acc gca act ggt gtt gcc aag gtg cac cag ctg	2832
Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu	
930 935 940	
gag gag aag cag ctt atc gac gag gct ttc gag gct taagtcttta	2878
Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala	
945 950 955	
tagtcctgca cta	2891

&lt;210&gt; 562

&lt;211&gt; 956

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 562

Arg His Ser Val Pro Arg Leu Thr Lys Gly Gln Gly Thr Ile Ile Gly  
 1 5 10 15  
 Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp  
 20 25 30  
 Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr  
 35 40 45  
 Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg  
 50 55 60  
 Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe  
 65 70 75 80  
 Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val  
 85 90 95  
 Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu  
 100 105 110  
 Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser  
 115 120 125  
 Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile  
 130 135 140  
 Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val  
 145 150 155 160  
 Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser  
 165 170 175  
 Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His  
 180 185 190  
 Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala  
 195 200 205  
 Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys  
 210 215 220  
 Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val  
 225 230 235 240  
 Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu  
 245 250 255  
 Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val  
 260 265 270  
 Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile  
 275 280 285  
 Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met  
 290 295 300  
 Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly

305	310	315	320
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val	325	330	335
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met	340	345	350
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp	355	360	365
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala	370	375	380
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly	385	390	395
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly	405	410	415
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp	420	425	430
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp	435	440	445
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg	450	455	460
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg	465	470	475
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr	485	490	495
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp	500	505	510
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	515	520	525
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu	530	535	540
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln	545	550	555
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	565	570	575
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His	580	585	590
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu	595	600	605
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu	610	615	620
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg	625	630	635
			640

Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala  
 645 650 655  
 Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn  
 660 665 670  
 Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met  
 675 680 685  
 Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala  
 690 695 700  
 Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile  
 705 710 715 720  
 Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys  
 725 730 735  
 Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His  
 740 745 750  
 Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser  
 755 760 765  
 Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu  
 770 775 780  
 Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr  
 785 790 795 800  
 Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp  
 805 810 815  
 Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val  
 820 825 830  
 Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu  
 835 840 845  
 Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile  
 850 855 860  
 Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile  
 865 870 875 880  
 Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val  
 885 890 895  
 Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His  
 900 905 910  
 Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg  
 915 920 925  
 Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu  
 930 935 940  
 Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala  
 945 950 955

<210> 563  
 <211> 1517  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1494)  
 <223> RXA01745

<400> 563  
 atc ctt gca gac gaa gac gac acc gtc gac gtc ggc gca gtc atc gcc 48  
 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala  
 1 5 10 15  
 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96  
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala  
 20 25 30  
 gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag 144  
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu  
 35 40 45  
 gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa 192  
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu  
 50 55 60  
 atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg 240  
 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp  
 65 70 75 80  
 ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag 288  
 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu  
 85 90 95  
 gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc 336  
 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly  
 100 105 110  
 acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc 384  
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly  
 115 120 125  
 gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc 432  
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala  
 130 135 140  
 gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag 480  
 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu  
 145 150 155 160  
 cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct 528  
 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala  
 165 170 175  
 act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac 576  
 Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn  
 180 185 190  
 gtt cca tac gtc acc cca ctg gtg cgc aag ctt gct gaa aag cac ggc 624

Val	Pro	Tyr	Val	Thr	Pro	Leu	Val	Arg	Lys	Leu	Ala	Glu	Lys	His	Gly	
	195						200					205				
gtt	gac	ttg	aac	acc	gtg	acc	ggg	acc	ggg	atc	ggg	ggc	cgt	atc	cgc	672
Val	Asp	Leu	Asn	Thr	Val	Thr	Gly	Thr	Gly	Ile	Gly	Gly	Arg	Ile	Arg	
	210					215					220					
aag	cag	gat	gtt	ttg	gct	gct	gcg	aac	ggc	gag	gct	gca	cct	gct	gag	720
Lys	Gln	Asp	Val	Leu	Ala	Ala	Ala	Asn	Gly	Glu	Ala	Ala	Pro	Ala	Glu	
	225				230					235					240	
gct	gct	gct	cct	gtt	tcc	gct	tgg	tcc	act	aag	tct	gtt	gac	cct	gag	768
Ala	Ala	Ala	Pro	Val	Ser	Ala	Trp	Ser	Thr	Lys	Ser	Val	Asp	Pro	Glu	
				245					250					255		
aag	gct	aag	ctc	cgt	ggg	acc	act	cag	aag	gtc	aac	cgc	atc	cgt	gag	816
Lys	Ala	Lys	Leu	Arg	Gly	Thr	Thr	Gln	Lys	Val	Asn	Arg	Ile	Arg	Glu	
			260					265					270			
atc	acc	gcg	atg	aag	acc	gtc	gag	gct	ctg	cag	att	tct	gct	cag	ctc	864
Ile	Thr	Ala	Met	Lys	Thr	Val	Glu	Ala	Leu	Gln	Ile	Ser	Ala	Gln	Leu	
			275				280					285				
acc	cag	ctg	cac	gag	gtc	gat	atg	act	cgc	gtt	gct	gag	ctg	cgt	aag	912
Thr	Gln	Leu	His	Glu	Val	Asp	Met	Thr	Arg	Val	Ala	Glu	Leu	Arg	Lys	
	290					295					300					
aag	aac	aag	ccc	gcg	ttc	atc	gag	aag	cac	ggg	gtg	aac	ctc	act	tac	960
Lys	Asn	Lys	Pro	Ala	Phe	Ile	Glu	Lys	His	Gly	Val	Asn	Leu	Thr	Tyr	
	305				310					315					320	
ctg	cca	ttc	ttc	gtg	aag	gca	gtt	gtc	gag	gct	ttg	gtt	tcc	cat	cca	1008
Leu	Pro	Phe	Phe	Val	Lys	Ala	Val	Val	Glu	Ala	Leu	Val	Ser	His	Pro	
				325					330					335		
aac	gtc	aac	gcg	tct	ttc	aac	gcg	aag	acc	aag	gag	atg	acc	tac	cac	1056
Asn	Val	Asn	Ala	Ser	Phe	Asn	Ala	Lys	Thr	Lys	Glu	Met	Thr	Tyr	His	
			340					345					350			
tcc	tcc	gtt	aac	ctc	tcc	atc	gct	gtt	gat	acc	cca	gct	ggg	ctg	ttg	1104
Ser	Ser	Val	Asn	Leu	Ser	Ile	Ala	Val	Asp	Thr	Pro	Ala	Gly	Leu	Leu	
			355				360					365				
acc	cca	gtc	att	cac	gat	gct	cag	gat	ctc	tcc	atc	cca	gag	atc	gca	1152
Thr	Pro	Val	Ile	His	Asp	Ala	Gln	Asp	Leu	Ser	Ile	Pro	Glu	Ile	Ala	
	370					375					380					
aag	gca	att	gtt	gac	ctg	gct	gat	cgt	tca	cgc	aac	aac	aag	ctg	aag	1200
Lys	Ala	Ile	Val	Asp	Leu	Ala	Asp	Arg	Ser	Arg	Asn	Asn	Lys	Leu	Lys	
	385				390					395					400	
cca	aac	gat	ctg	tcc	ggg	ggc	acc	ttc	acc	atc	acc	aac	att	ggg	tct	1248
Pro	Asn	Asp	Leu	Ser	Gly	Gly	Thr	Phe	Thr	Ile	Thr	Asn	Ile	Gly	Ser	
				405					410					415		
gaa	ggc	gca	ctg	tct	gat	acc	cca	atc	ctg	gtt	cca	cca	cag	gct	ggc	1296
Glu	Gly	Ala	Leu	Ser	Asp	Thr	Pro	Ile	Leu	Val	Pro	Pro	Gln	Ala	Gly	
			420					425					430			
atc	ttg	ggc	acc	ggc	gcg	atc	gtg	aag	cgt	cca	gtt	gtc	atc	acc	gag	1344
Ile	Leu	Gly	Thr	Gly	Ala	Ile	Val	Lys	Arg	Pro	Val	Val	Ile	Thr	Glu	

435                      440                      445  
 gat gga att gat tcc atc gcg atc cgt cag atg gtc ttc cta cca ctg 1392  
 Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu  
 450                      455                      460  
 acc tac gac cac cag gtt gta gat ggc gca gat gct ggt cgc ttc ctg 1440  
 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu  
 465                      470                      475                      480  
 acc acc atc aag gac cgc ctt gag acc gct aac ttc gaa ggc gat ctg 1488  
 Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu  
 485                      490                      495  
 cag ctc taagatctct gcaagttaaa acc 1517  
 Gln Leu

&lt;210&gt; 564

&lt;211&gt; 498

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 564

Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala  
 1                      5                      10                      15

Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala  
 20                      25                      30

Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu  
 35                      40                      45

Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu  
 50                      55                      60

Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp  
 65                      70                      75                      80

Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu  
 85                      90                      95

Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly  
 100                      105                      110

Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly  
 115                      120                      125

Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala  
 130                      135                      140

Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu  
 145                      150                      155                      160

Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala  
 165                      170                      175

Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn  
 180                      185                      190

Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly  
 195 200 205  
 Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg  
 210 215 220  
 Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu  
 225 230 235 240  
 Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu  
 245 250 255  
 Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu  
 260 265 270  
 Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu  
 275 280 285  
 Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys  
 290 295 300  
 Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr  
 305 310 315 320  
 Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro  
 325 330 335  
 Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His  
 340 345 350  
 Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu  
 355 360 365  
 Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala  
 370 375 380  
 Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys  
 385 390 395 400  
 Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser  
 405 410 415  
 Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly  
 420 425 430  
 Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu  
 435 440 445  
 Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu  
 450 455 460  
 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu  
 465 470 475 480  
 Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu  
 485 490 495  
 Gln Leu



<210> 565  
<211> 1005  
<212> DNA  
<213> *Corynebacterium glutamicum*

```
<220>  
<221> CDS  
<222> (101)..(982)  
<223> RXA00782
```

<400> 565															60	
gggtatggat	gcagcggctg	atcacgctgc	ccatttggcc	aatcttggcc	agcacggcca											115
gttcgcaacc	gctaattagt	taaggagcac	ctgtttaatc	atg	tct	att	ttt	ctc								5
				Met	Ser	Ile	Phe	Leu								
				1												
aat tca gat tcc cgc atc atc att cag ggc att acc ggt tcg gaa ggt																163
Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile Thr Gly Ser Glu Gly																
			10					15						20		
tca gag cat gcg cgt cga att tta gcc tct ggt gcg aag ctc gtg ggt																211
Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly Ala Lys Leu Val Gly																
			25					30						35		
ggc acc aac ccc cgc aaa gct ggg caa acc att ttg atc aat gac act																259
Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile Leu Ile Asn Asp Thr																
			40				45						50			
gag ttg cct gta ttt ggc act gtt aag gaa gca atg gag gaa acg ggt																307
Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala Met Glu Glu Thr Gly																
			55				60					65				
gcg gat gtc acc gta att ttc gtt cct cca gcc ttt gcc aaa gct gcg																355
Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala Phe Ala Lys Ala Ala																
			70			75				80					85	
atc att gaa gct atc gac gct cac atc cca ctg tgc gtg att att act																403
Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu Cys Val Ile Ile Thr																
					90				95						100	
gag ggc atc cca gtg cgt gac gct tct gag gcg tgg gct tat gcc aag																451
Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala Trp Ala Tyr Ala Lys																
			105					110						115		
aag gtg gga cac acc cgc atc att ggc cct aac tgc cca ggc att att																499
Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn Cys Pro Gly Ile Ile																
			120				125						130			
act ccc ggc gaa tct ctt gcg gga att acg ccg gca aac att gca ggt																547
Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro Ala Asn Ile Ala Gly																
			135				140					145				
tcc ggc ccg atc ggg ttg atc tca aag tcg gga aca ctg act tat cag																595
Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln																
			150			155				160					165	
atg atg tac gaa ctt tca gat att ggc att tct acg gcg att ggt att																643
Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser Thr Ala Ile Gly Ile																
				170				175						180		

ggc ggt gac cca atc atc ggt aca acc cat atc gac gct ctg gag gcc 691  
 Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp Ala Leu Glu Ala  
                   185                                  190                                  195

ttt gaa gct gat cct gag acc aag gca atc gtc atg atc ggt gag atc 739  
 Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met Ile Gly Glu Ile  
                   200                                  205                                  210

ggt gga gat gca gag gaa cgc gct gct gac ttc att tct aag cac gtg 787  
 Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile Ser Lys His Val  
                   215                                  220                                  225

aca aaa cca gtt gtg ggt tac gtg gca ggc ttt acc gcc cct gaa gga 835  
 Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly  
                   230                                  235                                  240                                  245

aag acc atg ggg cat gct ggc gcc atc gtg aca ggt tca gaa ggc act 883  
 Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr  
                   250                                  255                                  260

gcg cga gca aag aag cat gca ttg gag gcc gtg ggt gtt cgc gtg gga 931  
 Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly  
                   265                                  270                                  275

aca act ccg agt gaa acc gcg aag ctt atg cgt gag gta gtt gca gct 979  
 Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala  
                   280                                  285                                  290

ttg taactaacag gccacagatc tta 1005  
 Leu

<210> 566

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 566

Met Ser Ile Phe Leu Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile  
   1                                  5                                  10                                  15

Thr Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly  
                   20                                  25                                  30

Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile  
                   35                                  40                                  45

Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala  
                   50                                  55                                  60

Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala  
                   65                                  70                                  75                                  80

Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu  
                   85                                  90                                  95

Cys Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala  
                   100                                  105                                  110

Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn

115	120	125
Cys Pro Gly Ile Ile Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro		
130	135	140
Ala Asn Ile Ala Gly Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly		
145	150	155
Thr Leu Thr Tyr Gln Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser		
165	170	175
Thr Ala Ile Gly Ile Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile		
180	185	190
Asp Ala Leu Glu Ala Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val		
195	200	205
Met Ile Gly Glu Ile Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe		
210	215	220
Ile Ser Lys His Val Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe		
225	230	235
Thr Ala Pro Glu Gly Lys Thr Met Gly His Ala Gly Ala Ile Val Thr		
245	250	255
Gly Ser Glu Gly Thr Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val		
260	265	270
Gly Val Arg Val Gly Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg		
275	280	285
Glu Val Val Ala Ala Leu		
290		

<210> 567  
 <211> 1395  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1372)  
 <223> RXA00783

<400> 567  
 aaagttccca aggggtgggg gctgagcacc acggatccaa tttgttgca atttgcaaag 60  
  
 tttacagtgt tagacttcac aatacgatca tattggtgag ttg aaa cac tta ctt 115  
 Leu Lys His Leu Leu  
 1 5  
  
 tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg 163  
 Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro  
 10 15 20  
  
 gaa atg gaa ttg gca gtg gat ctt ttt gaa tac caa gca cgg gac ctc 211  
 Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr Gln Ala Arg Asp Leu  
 25 30 35

ttt gaa acc cat ggt gtg cca gtg ttg aag gga att gtg gca tca aca	259
Phe Glu Thr His Gly Val Pro Val Leu Lys Gly Ile Val Ala Ser Thr	
40 45 50	
cca gag gcg gcg agg aaa gcg gct gag gaa atc ggc gga ctg acc gtc	307
Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Gly Leu Thr Val	
55 60 65	
gtc aag gct cag gtc aag gtg ggc gga cgt ggc aag gcg ggt ggc gtc	355
Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val	
70 75 80 85	
cgt gtg gca ccg acg tcg gct cag gct ttt gat gct gcg gat gcg att	403
Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile	
90 95 100	
ctc ggc atg gat atc aaa gga cac act gtt aat cag gtg atg gtg gcg	451
Leu Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala	
105 110 115	
cag ggc gct gac att gct gag gaa tac tat ttc tcc att ttg ttg gat	499
Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp	
120 125 130	
cgc gcg aat cgt tcg tat ctg gct atg tgc tct gtt gaa ggt ggc atg	547
Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met	
135 140 145	
gag atc gag atc ctg gcg aag gaa aag cct gaa gct ttg gca aag gtg	595
Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val	
150 155 160 165	
gaa gtg gat ccc ctc act ggt att gat gag gac aaa gcg cgg gag att	643
Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile	
170 175 180	
gtc act gct gct ggc ttt gaa act gag gtg gca gag aaa gtc att ccg	691
Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala Glu Lys Val Ile Pro	
185 190 195	
gtg ctg atc aag atc tgg cag gtg tat tac gaa gag gaa gca aca ctc	739
Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu	
200 205 210	
gtt gag gtg aac ccg ttg gtg ctc acg gat gac ggc gat gtg att gcg	787
Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala	
215 220 225	
ctt gat ggc aag atc acg ctg gat gat aac gct gat ttc cgc cat gat	835
Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp	
230 235 240 245	
aac cgt ggt gcg ttg gct gaa tct gcc ggt ggc ttg gac att ttg gaa	883
Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu	
250 255 260	
ctg aag gcc aag aag aat gat ctg aac tac gtg aaa ctt gat ggc tct	931
Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser	
265 270 275	
gtg ggc atc att ggc aat ggt gca ggt ttg gtg atg tcc acg ttg gat	979

Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp  
 280 285 290

atc gtg gct gca gct ggt gaa cgc cat ggt ggg cag cgc ccc gcg aac 1027  
 Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn  
 295 300 305

ttc cta gac att ggt ggc gga gca tca gct gaa tcg atg gct gct ggt 1075  
 Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly  
 310 315 320 325

ctc gat gtg atc ctt ggg gat agc cag gta cgc agt gtg ttt gtg aat 1123  
 Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn  
 330 335 340

gtg ttt ggt ggc atc acc gcg tgt gat gtg gtg gca aag gga atc gtt 1171  
 Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val  
 345 350 355

gga gct ttg gat gtg ctc ggc gat caa gca acg aag cct ctt gtg gtg 1219  
 Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val  
 360 365 370

cgc ctt gat ggc aac aac gtg gtg gaa ggc aga cga atc ctc gcg gaa 1267  
 Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu  
 375 380 385

tat aac cac cct ttg gtc acc gtt gtg gag ggt atg gat gca gcg gct 1315  
 Tyr Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala  
 390 395 400 405

gat cac gct gcc cat ttg gcc aat ctt gcc cag cac ggc cag ttc gca 1363  
 Asp His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala  
 410 415 420

acc gct aat tagttaagga gcacctgttt aat 1395  
 Thr Ala Asn

&lt;210&gt; 568

&lt;211&gt; 424

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 568

Leu Lys His Leu Leu Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly  
 1 5 10 15

Ser Lys His Gly Pro Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr  
 20 25 30

Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly  
 35 40 45

Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile  
 50 55 60

Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly  
 65 70 75 80

Lys	Ala	Gly	Gly	Val	Arg	Val	Ala	Pro	Thr	Ser	Ala	Gln	Ala	Phe	Asp	
				85					90					95		
Ala	Ala	Asp	Ala	Ile	Leu	Gly	Met	Asp	Ile	Lys	Gly	His	Thr	Val	Asn	
			100					105					110			
Gln	Val	Met	Val	Ala	Gln	Gly	Ala	Asp	Ile	Ala	Glu	Glu	Tyr	Tyr	Phe	
		115					120					125				
Ser	Ile	Leu	Leu	Asp	Arg	Ala	Asn	Arg	Ser	Tyr	Leu	Ala	Met	Cys	Ser	
	130					135					140					
Val	Glu	Gly	Gly	Met	Glu	Ile	Glu	Ile	Leu	Ala	Lys	Glu	Lys	Pro	Glu	
145					150					155					160	
Ala	Leu	Ala	Lys	Val	Glu	Val	Asp	Pro	Leu	Thr	Gly	Ile	Asp	Glu	Asp	
				165					170					175		
Lys	Ala	Arg	Glu	Ile	Val	Thr	Ala	Ala	Gly	Phe	Glu	Thr	Glu	Val	Ala	
			180					185						190		
Glu	Lys	Val	Ile	Pro	Val	Leu	Ile	Lys	Ile	Trp	Gln	Val	Tyr	Tyr	Glu	
		195					200					205				
Glu	Glu	Ala	Thr	Leu	Val	Glu	Val	Asn	Pro	Leu	Val	Leu	Thr	Asp	Asp	
	210					215					220					
Gly	Asp	Val	Ile	Ala	Leu	Asp	Gly	Lys	Ile	Thr	Leu	Asp	Asp	Asn	Ala	
225					230					235					240	
Asp	Phe	Arg	His	Asp	Asn	Arg	Gly	Ala	Leu	Ala	Glu	Ser	Ala	Gly	Gly	
				245					250					255		
Leu	Asp	Ile	Leu	Glu	Leu	Lys	Ala	Lys	Lys	Asn	Asp	Leu	Asn	Tyr	Val	
			260					265						270		
Lys	Leu	Asp	Gly	Ser	Val	Gly	Ile	Ile	Gly	Asn	Gly	Ala	Gly	Leu	Val	
		275					280					285				
Met	Ser	Thr	Leu	Asp	Ile	Val	Ala	Ala	Ala	Gly	Glu	Arg	His	Gly	Gly	
	290					295					300					
Gln	Arg	Pro	Ala	Asn	Phe	Leu	Asp	Ile	Gly	Gly	Gly	Ala	Ser	Ala	Glu	
305					310					315					320	
Ser	Met	Ala	Ala	Gly	Leu	Asp	Val	Ile	Leu	Gly	Asp	Ser	Gln	Val	Arg	
				325					330					335		
Ser	Val	Phe	Val	Asn	Val	Phe	Gly	Gly	Ile	Thr	Ala	Cys	Asp	Val	Val	
			340					345					350			
Ala	Lys	Gly	Ile	Val	Gly	Ala	Leu	Asp	Val	Leu	Gly	Asp	Gln	Ala	Thr	
		355					360					365				
Lys	Pro	Leu	Val	Val	Arg	Leu	Asp	Gly	Asn	Asn	Val	Val	Glu	Gly	Arg	
	370					375					380					
Arg	Ile	Leu	Ala	Glu	Tyr	Asn	His	Pro	Leu	Val	Thr	Val	Val	Glu	Gly	
385					390					395					400	
Met	Asp	Ala	Ala	Ala	Asp	His	Ala	Ala	His	Leu	Ala	Asn	Leu	Ala	Gln	

405

410

415

His Gly Gln Phe Ala Thr Ala Asn  
420

&lt;210&gt; 569

&lt;211&gt; 1623

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1600)

&lt;223&gt; RXN01695

&lt;400&gt; 569

tatggccaac acttgcatc ggggtgctggc gatcatttat gagatgacgc cttgtgttgg 60

tggtcggcag	agaactcgcg	gagataaaag	gaagttgaac	atg	tca	gat	tcc	ccg	115
				Met	Ser	Asp	Ser	Pro	
				1				5	

aag	aac	gca	ccg	agg	att	acc	gat	gag	gca	gat	gta	gtt	ctc	att	ggc	163
Lys	Asn	Ala	Pro	Arg	Ile	Thr	Asp	Glu	Ala	Asp	Val	Val	Leu	Ile	Gly	
				10				15					20			

gcc	ggc	atc	atg	agc	tcc	acg	ctg	ggc	gca	atg	ctg	cgt	cag	ctg	gag	211
Ala	Gly	Ile	Met	Ser	Ser	Thr	Leu	Gly	Ala	Met	Leu	Arg	Gln	Leu	Glu	
			25					30					35			

cca	agc	tgg	act	cag	atc	gtc	ttc	gag	cgt	ttg	gat	gga	ccg	gca	caa	259
Pro	Ser	Trp	Thr	Gln	Ile	Val	Phe	Glu	Arg	Leu	Asp	Gly	Pro	Ala	Gln	
		40				45						50				

gag	tgc	tcc	tcc	ccg	tgg	aac	aat	gca	gga	acc	ggc	cac	tct	gct	cta	307
Glu	Ser	Ser	Ser	Pro	Trp	Asn	Asn	Ala	Gly	Thr	Gly	His	Ser	Ala	Leu	
	55					60					65					

tgc	gag	ctg	aac	tac	acc	cca	gag	gtt	aag	ggc	aag	gtt	gaa	att	gcc	355
Cys	Glu	Leu	Asn	Tyr	Thr	Pro	Glu	Val	Lys	Gly	Lys	Val	Glu	Ile	Ala	
	70				75					80					85	

aag	gct	gta	gga	atc	aac	gag	aag	ttc	cag	gtt	tcc	cgt	cag	ttc	tgg	403
Lys	Ala	Val	Gly	Ile	Asn	Glu	Lys	Phe	Gln	Val	Ser	Arg	Gln	Phe	Trp	
				90				95						100		

tct	cac	ctc	gtt	gaa	gag	gga	gtg	ctg	tct	gat	cct	aag	gaa	ttc	atc	451
Ser	His	Leu	Val	Glu	Glu	Gly	Val	Leu	Ser	Asp	Pro	Lys	Glu	Phe	Ile	
			105					110					115			

aac	cct	gtt	cct	cac	gta	tct	ttc	ggc	cag	ggc	gca	gat	cag	gtt	gca	499
Asn	Pro	Val	Pro	His	Val	Ser	Phe	Gly	Gln	Gly	Ala	Asp	Gln	Val	Ala	
		120					125					130				

tac	atc	aag	gct	cgc	tac	gaa	gct	ttg	aag	gat	cac	cca	ctc	ttc	cag	547
Tyr	Ile	Lys	Ala	Arg	Tyr	Glu	Ala	Leu	Lys	Asp	His	Pro	Leu	Phe	Gln	
	135					140					145					

ggc	atg	acc	tac	gct	gac	gat	gaa	gct	acc	ttc	acc	gag	aag	ctg	cct	595
Gly	Met	Thr	Tyr	Ala	Asp	Asp	Glu	Ala	Thr	Phe	Thr	Glu	Lys	Leu	Pro	

150	155	160	165	
ttg atg gca aag	ggc cgt gac ttc tct	gat cca gta gca atc	tct tgg	643
Leu Met Ala Lys	Gly Arg Asp Phe Ser	Asp Pro Val Ala Ile	Ser Trp	
	170	175	180	
atc gat gaa ggc	acc gac atc aac tac	ggg gct cag acc aag	cag tac	691
Ile Asp Glu Gly	Thr Asp Ile Asn Tyr	Gly Ala Gln Thr Lys	Gln Tyr	
	185	190	195	
ctg gat gca gct	gaa gtt gaa ggc	act gaa atc cgc	tat ggc cac gaa	739
Leu Asp Ala Ala	Glu Val Glu Gly	Thr Glu Ile Arg	Tyr Gly His Glu	
	200	205	210	
gtc aag agc atc	aag gct gat ggc	gca aag tgg atc	gtg acc gtc aag	787
Val Lys Ser Ile	Lys Ala Asp Gly	Ala Lys Trp Ile	Val Thr Val Lys	
	215	220	225	
aac gta cac act	ggc gac acc aag acc	atc aag gca aac	ttc gtg ttc	835
Asn Val His Thr	Gly Asp Thr Lys Thr	Ile Lys Ala Asn	Phe Val Phe	
	230	235	240	245
gtc ggc gca ggc	gga tac gca ctg	gat ctg ctt cgc	agc gca ggc atc	883
Val Gly Ala Gly	Gly Tyr Ala Leu	Asp Leu Leu Arg	Ser Ala Gly Ile	
	250	255	260	
cca cag gtc aag	ggc ttc gct gga	ttc cca gta tcc	ggc ctg tgg ctt	931
Pro Gln Val Lys	Gly Phe Ala Gly	Phe Pro Val Ser	Gly Leu Trp Leu	
	265	270	275	
cgt tgc acc aac	gag gaa ctg atc	gag cag cac gca	gcc aag gta tat	979
Arg Cys Thr Asn	Glu Glu Leu Ile	Glu Gln His Ala	Ala Lys Val Tyr	
	280	285	290	
ggc aag gca tct	gtt ggc gct cct	cca atg tct gtt	cct cac ctt gac	1027
Gly Lys Ala Ser	Val Gly Ala Pro	Pro Met Ser Val	Pro His Leu Asp	
	295	300	305	
acc cgc gtt atc	gag ggt gaa aag	ggt ctg ctc ttt	gga cct tac ggt	1075
Thr Arg Val Ile	Glu Gly Glu Lys	Gly Leu Leu Phe	Gly Pro Tyr Gly	
	310	315	320	325
ggc tgg acc cct	aag ttc ttg aag	gaa ggc tcc tac	ctg gac ctg ttc	1123
Gly Trp Thr Pro	Lys Phe Leu Lys	Glu Gly Ser Tyr	Leu Asp Leu Phe	
	330	335	340	
aag tcc atc cgc	cca gac aac att	cct tcc tac ctt	ggc gtt gct gct	1171
Lys Ser Ile Arg	Pro Asp Asn Ile	Pro Ser Tyr Leu	Gly Val Ala Ala	
	345	350	355	
cag gaa ttt gat	ctg acc aag tac	ctt gtc act gaa	gtt ctc aag gac	1219
Gln Glu Phe Asp	Leu Thr Lys Tyr	Leu Val Thr Glu	Val Leu Lys Asp	
	360	365	370	
cag gac aag cgt	atg gat gct ctt	cgc gag tac atg	cca gag gca caa	1267
Gln Asp Lys Arg	Met Asp Ala Leu	Arg Glu Tyr Met	Pro Glu Ala Gln	
	375	380	385	
aac ggc gat tgg	gag acc atc gtt	gcc gga cag cgt	gtt cag gtt att	1315
Asn Gly Asp Trp	Glu Thr Ile Val	Ala Gly Gln Arg	Val Gln Val Ile	
	390	395	400	405



aag cct gca gga ttc cct aag ttc ggt tcc ctg gaa ttc ggc acc acc 1363  
 Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu Glu Phe Gly Thr Thr  
 410 415 420  
 ttg atc aac aac tcc gaa ggc acc atc gcc gga ttg ctc ggt gct tcc 1411  
 Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly Leu Leu Gly Ala Ser  
 425 430 435  
 cct gga gca tcc atc gca cct tcc gca atg atc gag ctg ctt gag cgt 1459  
 Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile Glu Leu Leu Glu Arg  
 440 445 450  
 tgc ttc ggt gac cgc atg atc gag tgg ggc gac aag ctg aag gac atg 1507  
 Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp Lys Leu Lys Asp Met  
 455 460 465  
 atc cct tcc tac ggc aag aag ctt gct tcc gag cca gca ctg ttt gag 1555  
 Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu Pro Ala Leu Phe Glu  
 470 475 480 485  
 cag cag tgg gca cgc acc cag aag acc ctg aag ctt gag gaa gcc 1600  
 Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys Leu Glu Glu Ala  
 490 495 500  
 taaatcttct aactgctttc ttt 1623

<210> 570  
 <211> 500  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 570  
 Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp  
 1 5 10 15  
 Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met  
 20 25 30  
 Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu  
 35 40 45  
 Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr  
 50 55 60  
 Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly  
 65 70 75 80  
 Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val  
 85 90 95  
 Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp  
 100 105 110  
 Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly  
 115 120 125  
 Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp  
 130 135 140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe  
 145 150 155 160  
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro  
 165 170 175  
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala  
 180 185 190  
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile  
 195 200 205  
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp  
 210 215 220  
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys  
 225 230 235 240  
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu  
 245 250 255  
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val  
 260 265 270  
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His  
 275 280 285  
 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser  
 290 295 300  
 Val Pro His Leu Asp Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu  
 305 310 315 320  
 Phe Gly Pro Tyr Gly Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser  
 325 330 335  
 Tyr Leu Asp Leu Phe Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr  
 340 345 350  
 Leu Gly Val Ala Ala Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr  
 355 360 365  
 Glu Val Leu Lys Asp Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr  
 370 375 380  
 Met Pro Glu Ala Gln Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln  
 385 390 395 400  
 Arg Val Gln Val Ile Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu  
 405 410 415  
 Glu Phe Gly Thr Thr Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly  
 420 425 430  
 Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile  
 435 440 445  
 Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp  
 450 455 460  
 Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu



ggc atg acc tac gct gac gat gaa gct acc ttc acc gag aag ctg cct 595  
 Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro  
 150 155 160 165

ttg atg gca aag ggc cgt gac ttc tct gat cca gta gca atc tct tgg 643  
 Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp  
 170 175 180

atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac 691  
 Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr  
 185 190 195

ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa 739  
 Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu  
 200 205 210

gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag 787  
 Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys  
 215 220 225

aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc 835  
 Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe  
 230 235 240 245

gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc 883  
 Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile  
 250 255 260

cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt 931  
 Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu  
 265 270 275

cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat 979  
 Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr  
 280 285 290

ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac 1027  
 Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp  
 295 300 305

acc cgc gtt atc 1039  
 Thr Arg Val Ile  
 310

&lt;210&gt; 572

&lt;211&gt; 313

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 572

Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp  
 1 5 10 15

Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met  
 20 25 30

Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu  
 35 40 45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr  
 50 55 60  
 Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly  
 65 70 75 80  
 Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val  
 85 90 95  
 Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp  
 100 105 110  
 Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly  
 115 120 125  
 Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp  
 130 135 140  
 His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe  
 145 150 155 160  
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro  
 165 170 175  
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala  
 180 185 190  
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile  
 195 200 205  
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp  
 210 215 220  
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys  
 225 230 235 240  
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu  
 245 250 255  
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val  
 260 265 270  
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His  
 275 280 285  
 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser  
 290 295 300  
 Val Pro His Leu Asp Thr Arg Val Ile  
 305 310

&lt;210&gt; 573

&lt;211&gt; 233

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(210)

&lt;223&gt; FRXA01695

&lt;400&gt; 573

gcc gga ttg ctc ggt gct tcc cct gga gca tcc atc gca cct tcc gca 48  
 Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala  
 1 5 10 15

atg atc gag ctg ctt gag cgt tgc ttc ggt gac cgc atg atc gag tgg 96  
 Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp  
 20 25 30

ggc gac aag ctg aag gac atg atc cct tcc tac ggc aag aag ctt gct 144  
 Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala  
 35 40 45

tcc gag cca gca ctg ttt gag cag cag tgg gca cgc acc cag aag acc 192  
 Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr  
 50 55 60

ctg aag ctt gag gaa gcc taaatcttct aactgctttc ttt 233  
 Leu Lys Leu Glu Glu Ala  
 65 70

&lt;210&gt; 574

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 574

Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala  
 1 5 10 15

Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp  
 20 25 30

Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala  
 35 40 45

Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr  
 50 55 60

Leu Lys Leu Glu Glu Ala  
 65 70

&lt;210&gt; 575

&lt;211&gt; 1063

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1063)

&lt;223&gt; RXA00290

&lt;400&gt; 575

agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115  
 Met Thr Ile Asp Leu  
 1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac	163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His	
10 15 20	
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883  
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly  
                           250                          255                          260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931  
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala  
                           265                          270                          275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979  
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro  
                           280                          285                          290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027  
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val  
                           295                          300                          305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063  
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser  
                           310                          315                          320

&lt;210&gt; 576

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 576

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu  
   1                          5                          10                          15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg  
                           20                          25                          30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val  
                           35                          40                          45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr  
                           50                          55                          60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala  
   65                          70                          75                          80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met  
                           85                          90                          95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile  
                           100                          105                          110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile  
                           115                          120                          125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser  
                           130                          135                          140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp  
   145                          150                          155                          160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu  
                           165                          170                          175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp



180										185										190																			
Leu	Lys	Ile	Val	Ile	Ser	Gly	Ala	Gly	Ala	Ala	Gly	Val	Ala	Ala	Val																								
195										200										205																			
Asp	Met	Leu	Thr	Asn	Ala	Gly	Ala	Thr	Asp	Ile	Val	Val	Leu	Asp	Ser																								
210										215										220																			
Arg	Gly	Ile	Ile	His	Asp	Ser	Arg	Glu	Asp	Leu	Ser	Pro	Val	Lys	Ala																								
225										230										235										240									
Ala	Leu	Ala	Glu	Lys	Thr	Asn	Pro	Arg	Gly	Ile	Ser	Gly	Gly	Ile	Asn																								
245										250										255																			
Glu	Ala	Phe	Thr	Gly	Ala	Asp	Leu	Phe	Ile	Gly	Val	Ser	Gly	Gly	Asn																								
260										265										270																			
Ile	Gly	Glu	Asp	Ala	Leu	Lys	Leu	Met	Ala	Pro	Glu	Pro	Ile	Leu	Phe																								
275										280										285																			
Thr	Leu	Ala	Asn	Pro	Thr	Pro	Glu	Ile	Asp	Pro	Glu	Leu	Ser	Gln	Lys																								
290										295										300																			
Tyr	Gly	Ala	Ile	Val	Ala	Thr	Gly	Pro	Val	Leu	Thr	Cys	Leu	Thr	Arg																								
305										310										315										320									

Ser

<210> 577  
 <211> 1347  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1324)  
 <223> RXN01048

<400> 577  
 agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60  
 gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115  
 Met Thr Ile Asp Leu 5  
 1  
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163  
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His 20  
 10 15  
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211  
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met 35  
 25 30  
 cgc gat cit tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259  
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu 50  
 40 45  
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307  
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly

55	60	65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly 70 75 80 85			355
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln 90 95 100			403
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp 105 110 115			451
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro 120 125 130			499
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe 135 140 145			547
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His 150 155 160 165			595
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn 170 175 180			643
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile 185 190 195			691
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn 200 205 210			739
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His 215 220 225			787
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys 230 235 240 245			835
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly 250 255 260			883
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala 265 270 275			931
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro 280 285 290			979
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val 295 300 305			1027

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075  
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala  
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123  
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile  
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171  
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln  
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219  
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro  
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267  
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg  
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315  
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala  
 390 395 400 405

cca ata ttt taagagcaaa cttgaggccc aca 1347  
 Pro Ile Phe

&lt;210&gt; 578

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 578

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu  
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg  
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val  
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr  
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala  
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met  
 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile  
 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile  
 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser

130	135	140
Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp		
145	150	155 160
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu		
	165	170 175
Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp		
	180	185 190
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val		
	195	200 205
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser		
	210	215 220
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala		
	225	230 235 240
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn		
	245	250 255
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn		
	260	265 270
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe		
	275	280 285
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys		
	290	295 300
Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile		
	305	310 315 320
Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala		
	325	330 335
Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln		
	340	345 350
Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu		
	355	360 365
Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg		
	370	375 380
Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser		
	385	390 395 400
Leu Pro Val Glu Ala Pro Ile Phe		
	405	

&lt;210&gt; 579

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(288)

&lt;223&gt; FRXA01048

&lt;400&gt; 579

```

cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga      48
Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1              5              10              15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag      96
Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
              20              25              30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc      144
Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
              35              40              45

tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc      192
Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
              50              55              60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt      240
Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
              65              70              75              80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt      288
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
              85              90              95

taagagcaaa cttgaggccc aca      311

```

&lt;210&gt; 580

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 580

```

Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1              5              10              15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
              20              25              30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
              35              40              45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
              50              55              60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
              65              70              75              80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
              85              90              95

```

&lt;210&gt; 581

&lt;211&gt; 1063

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1063)

&lt;223&gt; FRXA00290

&lt;400&gt; 581

```

agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
                               Met Thr Ile Asp Leu
                               1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
                               10 15 20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
                               25 30 35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
                               40 45 50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
                               55 60 65

aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
                               70 75 80 85

gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
                               90 95 100

ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
                               105 110 115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
                               120 125 130

tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc 547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
                               135 140 145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
                               150 155 160 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
                               170 175 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att 691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile

```

185										190					195					
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739																			
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn																				
200 205 210																				
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787																			
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His																				
215 220 225																				
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835																			
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys																				
230 235 240 245																				
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883																			
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly																				
250 255 260																				
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct	931																			
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala																				
265 270 275																				
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca	979																			
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro																				
280 285 290																				
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc	1027																			
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val																				
295 300 305																				
gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca	1063																			
Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser																				
310 315 320																				

&lt;210&gt; 582

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 582

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu	
1 5 10 15	
Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg	
20 25 30	
Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val	
35 40 45	
Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr	
50 55 60	
His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala	
65 70 75 80	
Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met	
85 90 95	
Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile	
100 105 110	

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile  
 115 120 125  
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser  
 130 135 140  
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp  
 145 150 155 160  
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu  
 165 170 175  
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp  
 180 185 190  
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val  
 195 200 205  
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser  
 210 215 220  
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala  
 225 230 235 240  
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn  
 245 250 255  
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn  
 260 265 270  
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe  
 275 280 285  
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys  
 290 295 300  
 Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg  
 305 310 315 320  
 Ser

<210> 583  
 <211> 582  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(582)  
 <223> RXN03101

<400> 583  
 atc ctt gca gac gaa gac gac acc gtc gac gtc ggc gca gtc atc gcc 48  
 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala  
 1 5 10 15  
 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96  
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala



20	25	30	
gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu 35 40 45			144
gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu 50 55 60			192
atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp 65 70 75 80			240
ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu 85 90 95			288
gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly 100 105 110			336
acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly 115 120 125			384
gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala 130 135 140			432
gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Pro Val Lys Glu Glu 145 150 155 160			480
cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala 165 170 175			528
act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn 180 185 190			576
gtt cca Val Pro			582

&lt;210&gt; 584

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 584

Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala  
1 5 10 15

Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala  
20 25 30

Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu  
35 40 45

Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu  
 50 55 60

Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp  
 65 70 75 80

Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu  
 85 90 95

Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly  
 100 105 110

Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly  
 115 120 125

Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala  
 130 135 140

Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu  
 145 150 155 160

Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala  
 165 170 175

Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn  
 180 185 190

Val Pro

&lt;210&gt; 585

&lt;211&gt; 540

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(517)

&lt;223&gt; RXN02046

&lt;400&gt; 585

tccgtgccat caccaccggc gagatcactg gcatcgtgga cgcaaaacaa acagcaacag 60

aaattattaa catccgacgc aacgcttcag gagagtcctc atg aaa gag aca ctg 115  
 Met Lys Glu Thr Leu  
 1 5

acc acc ggt tta acc cac caa atg acc tac ata gtg cca gca aac cgc 163  
 Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile Val Pro Ala Asn Arg  
 10 15 20

aca gtt ccg cat ctg ctt ccc gaa gca gca gaa ttt gaa acc atg cca 211  
 Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu Phe Glu Thr Met Pro  
 25 30 35

gat gtc ctg gcc act gga tat atg gtc ggc atc atc gag tgg gcc tgc 259  
 Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile Ile Glu Trp Ala Cys  
 40 45 50

atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg ggc 307  
 Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly  
 55 60 65  
 act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg 355  
 Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr  
 70 75 80 85  
 gtc acc atc gat gtt gag gtg aca gag atc aac cgt cgt gca gtt acc 403  
 Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn Arg Arg Ala Val Thr  
 90 95 100  
 ttc aac atc act gca gct gat gag ttc gcc acc atc agc acc ggc acc 451  
 Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr Ile Ser Thr Gly Thr  
 105 110 115  
 cac cag cgc ggt gtg gtt aac cgt gag aag ttt gtc tcc cgt ctg cct 499  
 His Gln Arg Gly Val Val Asn Arg Glu Lys Phe Val Ser Arg Leu Pro  
 120 125 130  
 gaa gca cct aag gaa aac taaatcatgg ccaagttggt tga 540  
 Glu Ala Pro Lys Glu Asn  
 135

&lt;210&gt; 586

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 586

Met Lys Glu Thr Leu Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile  
 1 5 10 15  
 Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu  
 20 25 30  
 Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile  
 35 40 45  
 Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly  
 50 55 60  
 Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr  
 65 70 75 80  
 Val Pro Gly Ser Thr Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn  
 85 90 95  
 Arg Arg Ala Val Thr Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr  
 100 105 110  
 Ile Ser Thr Gly Thr His Gln Arg Gly Val Val Asn Arg Glu Lys Phe  
 115 120 125  
 Val Ser Arg Leu Pro Glu Ala Pro Lys Glu Asn  
 130 135

&lt;210&gt; 587

&lt;211&gt; 1683

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1660)

&lt;223&gt; RXN00389

&lt;400&gt; 587

```

ccaccactgc gtaacctttc cgagcaagat atcgcgacc tgctcgattt gcttgccacc 60
tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115
                                         Met Ile Thr Ala Thr
                                         1           5
gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
                        10                15                20
aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
                        25                30                35
cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259
Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu Arg Ala Ala Thr Thr
                        40                45                50
tcg gcg aag cga gct ttt gaa agc tac cga ctc act act cca gag gtt 307
Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu Thr Thr Pro Glu Val
                        55                60                65
aga gca gat ttc ctg gat tcc atc gct gac aac atc gat gcg cta tcc 355
Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn Ile Asp Ala Leu Ser
                        70                75                80                85
ggc gag atc gtg caa cgg gcg agc ctg gag aca ggt ttg gga act acc 403
Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr Gly Leu Gly Thr Thr
                        90                95                100
cga ctc aca ggc gaa gta gcc cgc acc agc aac cag ctc cgc ctg ttt 451
Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn Gln Leu Arg Leu Phe
                        105                110                115
gca gaa acc gtg aga agc gga cag ttc cac cga gta cgc att gaa cga 499
Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg Val Arg Ile Glu Arg
                        120                125                130
gga ccg cgg att gat ctt cgc cag cgt cag gtt ccg ttg gga cca gtc 547
Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val Pro Leu Gly Pro Val
                        135                140                145
gcg gta ttc ggg gca agc aac ttc ccc gtc gct ttc tct act gct ggt 595
Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala Phe Ser Thr Ala Gly
                        150                155                160                165
ggc gat aca gca tca gcg ttg gct gca ggc tgc cct gtg gtt ttt aag 643
Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys Pro Val Val Phe Lys
                        170                175                180
gcg cat aat gcg cac cct gga aca gct gag ctc gtc ggg caa gcg gtg 691
Ala His Asn Ala His Pro Gly Thr Ala Glu Leu Val Gly Gln Ala Val

```

185					190					195					
cgg gga gcc gtc gaa aag cat gag ttt gat gct ggt gtg ttt aac ctt	739														
Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala Gly Val Phe Asn Leu															
200	205					210									
gtc tac ggc cgt ggc gtg gaa att ggc cag gag ctg gct gcg gat ccg	787														
Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu Leu Ala Ala Asp Pro															
215	220					225									
aat atc acg gca atc ggt ttt acc ggt tca cgc cag ggt ggt ttg gca	835														
Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg Gln Gly Gly Leu Ala															
230	235					240					245				
ctg tca cag act gcg ttt agc cgc cca gtt ccc gtt cca gtc ttt gca	883														
Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro Val Pro Val Phe Ala															
250	255					260									
gaa atg agt gcc acc aac cct gtg ttc gtc ttc ccc ggc gcg ctg gcg	931														
Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe Pro Gly Ala Leu Ala															
265	270					275									
gat ttg gat gca tcg agt tcc ttg gct gag gcg ttt acc gct tcc gtc	979														
Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala Phe Thr Ala Ser Val															
280	285					290									
acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc	1027														
Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile															
295	300					305									
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa	1075														
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys															
310	315					320					325				
ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag	1123														
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln															
330	335					340									
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa	1171														
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys															
345	350					355									
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg	1219														
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro															
360	365					370									
gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg	1267														
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu															
375	380					385									
cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc	1315														
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser															
390	395					400					405				
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca	1363														
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr															
410	415					420									
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt	1411														
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu															
425	430					435									

atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459  
 Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp  
           440                          445                          450  
  
 cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507  
 Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr  
           455                          460                          465  
  
 ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555  
 Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile  
           470                          475                          480                          485  
  
 gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg 1603  
 Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu  
                           490                          495                          500  
  
 ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa 1651  
 Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu  
                           505                          510                          515  
  
 ata gac cgt taatagctgg tctttacatt tgc 1683  
 Ile Asp Arg  
           520

<210> 588  
 <211> 520  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 588  
 Met Ile Thr Ala Thr Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu  
       1                          5                          10                          15  
  
 Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr  
           20                          25                          30  
  
 Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu  
           35                          40                          45  
  
 Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu  
           50                          55                          60  
  
 Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn  
           65                          70                          75                          80  
  
 Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr  
                           85                          90                          95  
  
 Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn  
           100                          105                          110  
  
 Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg  
           115                          120                          125  
  
 Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val  
           130                          135                          140  
  
 Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala  
           145                          150                          155                          160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys  
 165 170 175  
 Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu  
 180 185 190  
 Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala  
 195 200 205  
 Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu  
 210 215 220  
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg  
 225 230 235 240  
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro  
 245 250 255  
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe  
 260 265 270  
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala  
 275 280 285  
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro  
 290 295 300  
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala  
 305 310 315 320  
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr  
 325 330 335  
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala  
 340 345 350  
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu  
 355 360 365  
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu  
 370 375 380  
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val  
 385 390 395 400  
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu  
 405 410 415  
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln  
 420 425 430  
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val  
 435 440 445  
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile  
 450 455 460  
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val  
 465 470 475 480

<400> 589																
ttgacgcacc	aatgcccgat	ggagcaatgt	gtgaaccacg	ccaccacgca	aaccgatgca	60										
catcacgtcg	aaacagtgac	agtgacattag	ctcatacttt	gtg	gtc	ggc	acc	gcc	115							
				Val	Val	Gly	Thr	Ala								
				1				5								
cat	tgc	gaa	tca	gca	ctt	aag	gaa	gtg	act	ttg	atg	tca	aac	gtt	gga	163
His	Cys	Glu	Ser	Ala	Leu	Lys	Glu	Val	Thr	Leu	Met	Ser	Asn	Val	Gly	
				10				15						20		
aag	cca	cgt	acc	gca	cag	gaa	atc	cag	cag	gat	tgg	gac	acc	aac	cct	211
Lys	Pro	Arg	Thr	Ala	Gln	Glu	Ile	Gln	Gln	Asp	Trp	Asp	Thr	Asn	Pro	
			25					30					35			
cgt	tgg	aac	ggc	atc	acc	cgc	gac	tac	acc	gca	gac	cag	gta	gct	gat	259
Arg	Trp	Asn	Gly	Ile	Thr	Arg	Asp	Tyr	Thr	Ala	Asp	Gln	Val	Ala	Asp	
		40					45					50				
ctg	cag	ggt	tcc	gtc	atc	gag	gag	cac	act	ctt	gct	cgc	cgc	ggc	tca	307
Leu	Gln	Gly	Ser	Val	Ile	Glu	Glu	His	Thr	Leu	Ala	Arg	Arg	Gly	Ser	
		55				60					65					
gag	atc	ctc	tgg	gac	gca	gtc	acc	cag	gaa	ggt	gac	gga	tac	atc	aac	355
Glu	Ile	Leu	Trp	Asp	Ala	Val	Thr	Gln	Glu	Gly	Asp	Gly	Tyr	Ile	Asn	
	70				75					80					85	
gcg	ctt	ggc	gca	ctc	acc	ggt	aac	cag	gct	gtt	cag	cag	gtt	cgt	gca	403
Ala	Leu	Gly	Ala	Leu	Thr	Gly	Asn	Gln	Ala	Val	Gln	Gln	Val	Arg	Ala	
				90				95						100		
ggc	ctg	aag	gct	gtc	tac	ctg	tcc	ggt	tgg	cag	gtc	gca	ggt	gac	gcc	451
Gly	Leu	Lys	Ala	Val	Tyr	Leu	Ser	Gly	Trp	Gln	Val	Ala	Gly	Asp	Ala	
			105					110					115			
aac	ctc	tcc	ggc	cac	acc	tac	cct	gac	cag	tcc	ctc	tac	cca	gcg	aac	499
Asn	Leu	Ser	Gly	His	Thr	Tyr	Pro	Asp	Gln	Ser	Leu	Tyr	Pro	Ala	Asn	
		120					125					130				
ccc	gtt	cca	agc	gtc	gtt	cgt	cgc	atc	aac	aac	gca	ctg	ctg	cgt	tcc	547
Ser	Val	Pro	Ser	Val	Val	Arg	Arg	Ile	Asn	Asn	Ala	Leu	Leu	Arg	Ser	



135	140	145	
gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val 150 155 160 165			595
gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn 170 175 180			643
gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr 185 190 195			691
cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly 200 205 210			739
ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser 215 220 225			787
gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala 230 235 240 245			835
cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu 250 255 260			883
cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr 265 270 275			931
cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr 280 285 290			979
gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu 295 300 305			1027
gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp 310 315 320 325			1075
cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His 330 335 340			1123
ctc gag gca gat gag atc gct aag ttc cag aag gaa ctc ggc gca atg Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met 345 350 355			1171
ggc ttc aag ttc cag ttc atc acc ctc gca ggc ttc cac tcc ctc aac Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn 360 365 370			1219
tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr 375 380 385			1267

tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt 1315  
 Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg  
 390 395 400 405

ggc ttc acc gct gtt aag cac cag cgt gag gtt ggc gca ggc tac ttc 1363  
 Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe  
 410 415 420

gac cag atc gca acc acc gtt gac ccg aac tct tct acc acc gct ttg 1411  
 Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu  
 425 430 435

aag ggt tcc act gaa gaa ggc cag ttc cac aac taggacctac aggttctgac 1464  
 Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn  
 440 445

aat 1467

<210> 590

<211> 448

<212> PRT

<213> Corynebacterium glutamicum

<400> 590

Val Val Gly Thr Ala His Cys Glu Ser Ala Leu Lys Glu Val Thr Leu  
 1 5 10 15

Met Ser Asn Val Gly Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp  
 20 25 30

Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala  
 35 40 45

Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu  
 50 55 60

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly  
 65 70 75 80

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val  
 85 90 95

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln  
 100 105 110

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser  
 115 120 125

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn  
 130 135 140

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser  
 145 150 155 160

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe  
 165 170 175

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala  
 180 185 190

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys  
 195 200 205  
 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile  
 210 215 220  
 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro  
 225 230 235 240  
 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr  
 245 250 255  
 Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr  
 260 265 270  
 Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala  
 275 280 285  
 Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr  
 290 295 300  
 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg  
 305 310 315 320  
 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe  
 325 330 335  
 Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys  
 340 345 350  
 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly  
 355 360 365  
 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala  
 370 375 380  
 Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys  
 385 390 395 400  
 Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val  
 405 410 415  
 Gly Ala Gly Tyr Phe Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser  
 420 425 430  
 Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn  
 435 440 445

&lt;210&gt; 591

&lt;211&gt; 1419

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1396)

<400> 591

caccgcccatt tgcgaatcag cacttaagga agtgactttg atg tca aac gtt gga 115  
Met Ser Asn Val Gly  
1 5

aag cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cct 163  
Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro  
10 15 20

cgt tgg aac ggc atc acc cgc gac tac acc gca gac cag gta gct gat    211  
Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Asp Gln Val Ala Asp

25                          30                          35

ctg cag ggt tcc gtc atc gag gag cac act ctt gct cgc cgc ggc tca 259  
Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser  
40 45 50

gag atc ctc tgg gac gca gtc acc cag gaa ggt gac gga tac atc aac 307  
Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly Asp Gly Tyr Ile Asn  
55 60 65

gcg ctt ggc gca ctc acc ggt aac cag gct gtt cag cag gtt cgt gca 355  
Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala  
70 75 80 85

ggc ctg aag gct gtc tac ctg tcc ggt tgg cag gtc gca ggt gac gcc 403  
Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala  
90 95 100

aac ctc tcc ggc cac acc tac cct gac cag tcc ctc tac cca gcg aac 451  
Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn  
105 110 115

tcc gtt cca agc gtc gtt cgt cgc atc aac aac gca ctg ctg cgt tcc 499  
Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ser  
120 125 130

gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt 547  
Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val  
135 140 145

gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac 595  
Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn  
150 155 160 165

gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc 643  
Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr  
170 175 180

cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc 691  
 His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly  
 185 190 195

ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct 739  
Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser  
200 205 210

gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca	787
Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala	
215 220 225	
cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag	835
Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu	
230 235 240 245	
cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac	883
Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr	
250 255 260	
cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac	931
His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr	
265 270 275	
gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg	979
Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu	
280 285 290	
gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac	1027
Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp	
295 300 305	
cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac	1075
Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His	
310 315 320 325	
ctc gag gca gat gag atc gct aag ttc cag aag gaa ctc ggc gca atg	1123
Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met	
330 335 340	
ggc ttc aag ttc cag ttc atc acc ctc gca ggc ttc cac tcc ctc aac	1171
Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn	
345 350 355	
tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc	1219
Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr	
360 365 370	
tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt	1267
Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg	
375 380 385	
ggc ttc acc gct gtt aag cac cag cgt gag gtt ggc gca ggc tac ttc	1315
Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe	
390 395 400 405	
gac cag atc gca acc acc gtt gac ccg aac tct tct acc acc gct ttg	1363
Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu	
410 415 420	
aag ggt tcc act gaa gaa ggc cag ttc cac aac taggacctac aggttctgac	1416
Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn	
425 430	
aat	1419

&lt;210&gt; 592

&lt;211&gt; 432

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 592

Met Ser Asn Val Gly Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp  
 1 5 10 15

Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala  
 20 25 30

Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu  
 35 40 45

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly  
 50 55 60

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val  
 65 70 75 80

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln  
 85 90 95

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser  
 100 105 110

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn  
 115 120 125

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser  
 130 135 140

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe  
 145 150 155 160

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala  
 165 170 175

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys  
 180 185 190

Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile  
 195 200 205

Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro  
 210 215 220

Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr  
 225 230 235 240

Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr  
 245 250 255

Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala  
 260 265 270

Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr  
 275 280 285

Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg  
 290 295 300

Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe  
 305 310 315 320

Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys  
 325 330 335

Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly  
 340 345 350

Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala  
 355 360 365

Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys  
 370 375 380

Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val  
 385 390 395 400

Gly Ala Gly Tyr Phe Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser  
 405 410 415

Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn  
 420 425 430

&lt;210&gt; 593

&lt;211&gt; 2340

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2317)

&lt;223&gt; RXN02404

&lt;400&gt; 593

gttttcacaaa ccggttaacgg cgtagccaaa caagaaggat tcgcattctt ctgggttagg 60

cacaggtcat ctaaaaccca tgctttaaaa ggagccttca atg act gaa cag gaa 115  
 Met Thr Glu Gln Glu  
 1 5

ctg ttg tct gct cag act gcc gac aac gct gga act gac agc acc gaa 163  
 Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly Thr Asp Ser Thr Glu  
 10 15 20

cgc gtt gac gcg ggc gga atg cag gtt gca aaa gtt ctc tac gac ttt 211  
 Arg Val Asp Ala Gly Gly Met Gln Val Ala Lys Val Leu Tyr Asp Phe  
 25 30 35

gta acc gaa gcg gta ctc cct cgc gtg ggt gtg gat gcg gaa aag ttc 259  
 Val Thr Glu Ala Val Leu Pro Arg Val Gly Val Asp Ala Glu Lys Phe  
 40 45 50

tgg tcc gga ttc gcc gcc atc gcc cgg gac ctc acc cca cgc aac cgc 307  
 Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg  
 55 60 65

gag ctg ctt gct cgc cgc gat gaa ctg cag atg ctt atc gac gac tac	355
Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr	
70 75 80 85	
cac cgc aac aac tcc ggc acc atc gac caa gag gcg tac gag gat ttc	403
His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe	
90 95 100	
ctc aaa gaa atc gga tac ttg gtt gag gag cca gaa gct gca gaa atc	451
Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro Glu Ala Ala Glu Ile	
105 110 115	
cgt acc caa aac gtc gat acg gaa atc tcc agc acc gca gga cct cag	499
Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln	
120 125 130	
ctg gtt gtt cca att ctg aac gca cgc ttc gcg ctg aac gct gcc aat	547
Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn	
135 140 145	
gct cgc tgg ggt tcc ctc tac gat gcg ttg tac ggc acc aac gcc atc	595
Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile	
150 155 160 165	
cca gaa act gat ggc gct gaa aag ggc aag gag tac aac ccg gtc cgc	643
Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg	
170 175 180	
ggc cag aag gtc atc gag tgg ggt cgt gaa ttc ctc gac agc gtt gtc	691
Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe Leu Asp Ser Val Val	
185 190 195	
cca ctg gac ggt gct tcg cat gcc gat gtt gag aag tac aac atc acc	739
Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu Lys Tyr Asn Ile Thr	
200 205 210	
gat gga aag ctt gca gcc cac att gga gat agc gtc tac cga ctg aaa	787
Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser Val Tyr Arg Leu Lys	
215 220 225	
aac cgt gaa tcc tac cgt ggc ttc acc ggc aac ttc ctt gat cca gaa	835
Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu	
230 235 240 245	
gca atc ctg ctg gaa acc aac ggc ctg cac atc gag ctg cag atc gat	883
Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile Glu Leu Gln Ile Asp	
250 255 260	
cct gtc cac cca atc ggc aag gca gac aag act ggt ctc aaa gac atc	931
Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile	
265 270 275	
gtt ttg gaa tct gcg atc acc acg atc atg gac ttc gaa gac tcc gtt	979
Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp Phe Glu Asp Ser Val	
280 285 290	
gca gct gtt gat gct gaa gac aag acc tta ggt tac tct aac tgg ttc	1027
Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe	
295 300 305	
gga ctc aac acc ggc gaa ctg aaa gaa gag atg tcc aag aac gga cgc	1075



Gly 310	Leu	Asn	Thr	Gly 315	Glu	Leu	Lys	Glu	Glu	Met 320	Ser	Lys	Asn	Gly	Arg 325	
atc	ttc	acc	cgt	gag	ctc	aac	aag	gac	cgc	gtc	tac	att	ggc	cgc	aat	1123
Ile	Phe	Thr	Arg	Glu 330	Leu	Asn	Lys	Asp	Arg 335	Val	Tyr	Ile	Gly	Arg	Asn 340	
ggc	acc	gag	ctg	gtt	ctg	cac	ggt	cgt	tcc	ctg	ctg	ttc	gtc	cgc	aac	1171
Gly	Thr	Glu	Leu	Val 345	Leu	His	Gly	Arg 350	Ser	Leu	Leu	Phe	Val	Arg	Asn 355	
gtt	ggc	cac	ctc	atg	caa	aac	cca	tcc	atc	ttg	att	gat	ggc	gag	gag	1219
Val	Gly	His 360	Leu	Met	Gln	Asn	Pro 365	Ser	Ile	Leu	Ile	Asp	Gly	Glu	Glu 370	
atc	ttc	gaa	ggc	atc	atg	gat	gct	gtc	ttg	acc	act	gtt	tgt	gcc	atc	1267
Ile	Phe	Glu	Gly	Ile	Met	Asp	Ala 380	Val	Leu	Thr	Thr	Val	Cys	Ala	Ile 385	
cca	gga	att	gct	ccg	cag	aac	aag	atg	cgc	aat	tcc	cgc	aag	ggc	tcc	1315
Pro	Gly	Ile	Ala	Pro	Gln	Asn	Lys 395	Met	Arg	Asn 400	Ser	Arg	Lys	Gly	Ser 405	
atc	tac	atc	gtg	aag	cct	aag	cag	cac	ggc	cct	gaa	gaa	gtc	gcg	ttc	1363
Ile	Tyr	Ile	Val	Lys 410	Pro	Lys	Gln	His	Gly 415	Pro	Glu	Glu	Val	Ala	Phe 420	
acc	aac	gag	ctc	ttc	ggc	cgc	gtt	gag	gat	ctg	ctt	gat	ctg	cca	cgc	1411
Thr	Asn	Glu	Leu	Phe 425	Gly	Arg	Val	Glu 430	Asp	Leu	Leu	Asp	Leu	Pro	Arg 435	
cac	acc	ttg	aag	gtt	ggt	gtt	atg	gat	gag	gag	cgt	cgc	acg	tcc	gtg	1459
His	Thr	Leu	Lys	Val 440	Gly	Val	Met 445	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val 450	
aac	ctg	gat	gcc	agc	atc	atg	gaa	gtt	gct	gac	cgc	ttg	gca	ttc	atc	1507
Asn	Leu	Asp	Ala	Ser	Ile	Met	Glu 460	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile 465	
aac	act	ggc	ttc	ctg	gac	cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	1555
Asn	Thr	Gly	Phe	Leu	Asp 475	Arg	Thr	Gly	Asp	Glu 480	Ile	His	Thr	Ser	Met 485	
gaa	gca	ggc	gcc	atg	gtg	cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	1603
Glu	Ala	Gly	Ala	Met 490	Val	Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp 500	
aag	cag	gcc	tac	gag	aac	aac	aac	gtt	gat	gca	ggt	att	cag	cgt	ggt	1651
Lys	Gln	Ala	Tyr	Glu	Asn	Asn	Asn 510	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly 515	
ctt	cct	ggc	aag	gct	cag	atc	ggt	aag	ggc	atg	tgg	gcg	atg	act	gaa	1699
Leu	Pro	Gly	Lys	Ala	Gln	Ile	Gly 525	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu 530	
ctc	atg	gca	gaa	atg	ctg	gag	aag	aag	atc	ggc	cag	cca	cgc	gaa	ggc	1747
Leu	Met	Ala	Glu	Met	Leu	Glu	Lys 540	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly 545	
gcc	aac	act	gca	tgg	gtt	cct	tca	cca	act	ggt	gcg	acg	ctg	cac	gca	1795
Ala	Asn	Thr	Ala	Trp	Val	Pro	Ser	Pro	Thr	Gly	Ala	Thr	Leu	His	Ala	

550	555	560	565	
acg cac tac cac ttg gtt gat gtg ttc aag gtt caa gac gaa ctg cgt				1843
Thr His Tyr His Leu Val Asp Val Phe Lys Val Gln Asp Glu Leu Arg	570	575	580	
gct gcc ggc cgc cgc gac agc ctg cgc aac att ctc acc att tca acc				1891
Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr	585	590	595	
gca cca aac acc aat tgg tct gag gaa gag aag aag gaa gag atg gac				1939
Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys Lys Glu Glu Met Asp	600	605	610	
aac aac tgc cag tcc atc ctc gga tac gtt gtg cgc tgg gtt gag cac				1987
Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Glu His	615	620	625	
ggt gtt ggt tgc tcc aag gtt cca gac atc cat gac atc gac ctc atg				2035
Gly Val Gly Cys Ser Lys Val Pro Asp Ile His Asp Ile Asp Leu Met	630	635	640	645
gaa gac cgc gca acg ctg cgt att tcc tcg cag atg ctg gcc aac tgg				2083
Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Asn Trp	650	655	660	
atc cgc cat gat gtt gtc tcg aag gag cag gtc ttg gag tca ctg gaa				2131
Ile Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu	665	670	675	
cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac				2179
Arg Met Ala Val Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr	680	685	690	
cgc gat atg gcg ccg aag tac gac gcc tcc ctc gcc ttc cag gcg gct				2227
Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala	695	700	705	
aag gac ttg att ttc gaa ggc acc aag tcc cca tcg ggc tac acc gag				2275
Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu	710	715	720	725
ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac				2317
Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys Ala Lys Asn	730	735		
taagcacgct ttctgacgct tac				2340

&lt;210&gt; 594

&lt;211&gt; 739

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 594

Met	Thr	Glu	Gln	Glu	Leu	Leu	Ser	Ala	Gln	Thr	Ala	Asp	Asn	Ala	Gly
1					5				10					15	

Thr	Asp	Ser	Thr	Glu	Arg	Val	Asp	Ala	Gly	Gly	Met	Gln	Val	Ala	Lys
				20				25					30		

Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu Pro Arg Val Gly Val  
 35 40 45  
 Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu  
 50 55 60  
 Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met  
 65 70 75 80  
 Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu  
 85 90 95  
 Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro  
 100 105 110  
 Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser  
 115 120 125  
 Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala  
 130 135 140  
 Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr  
 145 150 155 160  
 Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu  
 165 170 175  
 Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe  
 180 185 190  
 Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu  
 195 200 205  
 Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser  
 210 215 220  
 Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn  
 225 230 235 240  
 Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile  
 245 250 255  
 Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr  
 260 265 270  
 Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp  
 275 280 285  
 Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly  
 290 295 300  
 Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu Leu Lys Glu Glu Met  
 305 310 315 320  
 Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val  
 325 330 335  
 Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu His Gly Arg Ser Leu  
 340 345 350  
 Leu Phe Val Arg Asn Val Gly His Leu Met Gln Asn Pro Ser Ile Leu

355	360	365
Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met Asp Ala Val Leu Thr 370 375 380		
Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln Asn Lys Met Arg Asn 385 390 395 400		
Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro Lys Gln His Gly Pro 405 410 415		
Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly Arg Val Glu Asp Leu 420 425 430		
Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly Val Met Asp Glu Glu 435 440 445		
Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile Met Glu Val Ala Asp 450 455 460		
Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu 465 470 475 480		
Ile His Thr Ser Met Glu Ala Gly Ala Met Val Arg Lys Ala Asp Met 485 490 495		
Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn Asn Asn Val Asp Ala 500 505 510		
Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln Ile Gly Lys Gly Met 515 520 525		
Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu Glu Lys Lys Ile Gly 530 535 540		
Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val Pro Ser Pro Thr Gly 545 550 555 560		
Ala Thr Leu His Ala Thr His Tyr His Leu Val Asp Val Phe Lys Val 565 570 575		
Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile 580 585 590		
Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys 595 600 605		
Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val 610 615 620		
Arg Trp Val Glu His Gly Val Gly Cys Ser Lys Val Pro Asp Ile His 625 630 635 640		
Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln 645 650 655		
Met Leu Ala Asn Trp Ile Arg His Asp Val Val Ser Lys Glu Gln Val 660 665 670		
Leu Glu Ser Leu Glu Arg Met Ala Val Val Val Asp Lys Gln Asn Ala 675 680 685		

Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu  
690 695 700

Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro  
705 710 715 720

Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys  
725 730 735

Ala Lys Asn

<210> 595

<211> 2159

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2136)

<223> FRXA02404

<400> 595

atg cag gtt gca aaa gtt ctc tac gac ttt gta acc gaa gcg gta ctc 48  
Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu  
1 5 10 15

cct cgc gtg ggt gtg gat gcg gaa aag ttc tgg tcc gga ttc gcc gcc 96  
Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala  
20 25 30

atc gcc cgg gac ctc acc cca cgc aac cgc gag ctg ctt gct cgc cgc 144  
Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg  
35 40 45

gat gaa ctg cag atg ctt atc gac gac tac cac cgc aac aac tcc ggc 192  
Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly  
50 55 60

acc atc gac caa gag gcg tac gag gat ttc ctc aaa gaa atc gga tac 240  
Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr  
65 70 75 80

ttg gtt gag gag cca gaa gct gca gaa atc cgt acc caa aac gtc gat 288  
Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp  
85 90 95

acg gaa atc tcc agc acc gca gga cct cag ctg gtt gtt cca att ctg 336  
Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu  
100 105 110

aac gca cgc ttc gcg ctg aac gct gcc aat gct cgc tgg ggt tcc ctc 384  
Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu  
115 120 125

tac gat gcg ttg tac ggc acc aac gcc atc cca gaa act gat ggc gct 432  
Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala  
130 135 140

gaa aag ggc aag gag tac aac ccg gtc cgc ggc cag aag gtc atc gag	480
Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu	
145 150 155 160	
tggt ggt cgt gaa ttc ctc gac agc gtt gtc cca ctg gac ggt gct tcg	528
Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser	
165 170 175	
cat gcc gat gtt gag aag tac aac atc acc gat gga aag ctt gca gcc	576
His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala	
180 185 190	
cac att gga gat agc gtc tac cga ctg aaa aac cgt gaa tcc tac cgt	624
His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg	
195 200 205	
ggc ttc acc ggc aac ttc ctt gat cca gaa gca atc ctg ctg gaa acc	672
Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr	
210 215 220	
aac ggc ctg cac atc gag ctg cag atc gat cct gtc cac cca atc ggc	720
Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly	
225 230 235 240	
aag gca gac aag act ggt ctc aaa gac atc gtt ttg gaa tct gcg atc	768
Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile	
245 250 255	
acc acg atc atg gac ttc gaa gac tcc gtt gca gct gtt gat gct gaa	816
Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu	
260 265 270	
gac aag acc tta ggt tac tct aac tgg ttc gga ctc aac acc ggc gaa	864
Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu	
275 280 285	
ctg aaa gaa gag atg tcc aag aac gga cgc atc ttc acc cgt gag ctc	912
Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu	
290 295 300	
aac aag gac cgc gtc tac att ggc cgc aat ggt acc gag ctg gtt ctg	960
Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu	
305 310 315 320	
cac ggt cgt tcc ctg ctg ttc gtc cgc aac gtt ggt cac ctc atg caa	1008
His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln	
325 330 335	
aac cca tcc atc ttg att gat ggc gag gag atc ttc gaa ggc atc atg	1056
Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met	
340 345 350	
gat gct gtc ttg acc act gtt tgt gcc atc cca gga att gct ccg cag	1104
Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln	
355 360 365	
aac aag atg cgc aat tcc cgc aag ggc tcc atc tac atc gtg aag cct	1152
Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro	
370 375 380	
aag cag cac ggc cct gaa gaa gtc gcg ttc acc aac gag ctc ttc ggc	1200

Lys	Gln	His	Gly	Pro	Glu	Glu	Val	Ala	Phe	Thr	Asn	Glu	Leu	Phe	Gly		
385					390					395					400		
cgc	gtt	gag	gat	ctg	ctt	gat	ctg	cca	cgc	cac	acc	ttg	aag	gtt	ggt	1248	
Arg	Val	Glu	Asp	Leu	Leu	Asp	Leu	Pro	Arg	His	Thr	Leu	Lys	Val	Gly		
				405				410						415			
gtt	atg	gat	gag	gag	cgt	cgc	acg	tcc	gtg	aac	ctg	gat	gcc	agc	atc	1296	
Val	Met	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val	Asn	Leu	Asp	Ala	Ser	Ile		
			420					425					430				
atg	gaa	gtt	gct	gac	cgc	ttg	gca	ttc	atc	aac	act	ggc	ttc	ctg	gac	1344	
Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile	Asn	Thr	Gly	Phe	Leu	Asp		
		435					440					445					
cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	gaa	gca	ggc	gcc	atg	gtg	1392	
Arg	Thr	Gly	Asp	Glu	Ile	His	Thr	Ser	Met	Glu	Ala	Gly	Ala	Met	Val		
		450				455					460						
cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	aag	cag	gcc	tac	gag	aac	1440	
Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp	Lys	Gln	Ala	Tyr	Glu	Asn		
465					470					475					480		
aac	aac	gtt	gat	gca	ggt	att	cag	cgt	ggt	ctt	cct	ggc	aag	gct	cag	1488	
Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly	Leu	Pro	Gly	Lys	Ala	Gln		
				485					490					495			
atc	ggt	aag	ggc	atg	tgg	gcg	atg	act	gaa	ctc	atg	gca	gaa	atg	ctg	1536	
Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu	Leu	Met	Ala	Glu	Met	Leu		
			500					505					510				
gag	aag	aag	atc	ggc	cag	cca	cgc	gaa	ggc	gcc	aac	act	gca	tgg	gtt	1584	
Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly	Ala	Asn	Thr	Ala	Trp	Val		
		515					520					525					
cct	tca	cca	act	ggt	gcg	acg	ctg	cac	gca	acg	cac	tac	cac	ttg	gtt	1632	
Pro	Ser	Pro	Thr	Gly	Ala	Thr	Leu	His	Ala	Thr	His	Tyr	His	Leu	Val		
		530					535				540						
gat	gtg	ttc	aag	gtt	caa	gac	gaa	ctg	cgt	gct	gcc	ggc	cgc	cgc	gac	1680	
Asp	Val	Phe	Lys	Val	Gln	Asp	Glu	Leu	Arg	Ala	Ala	Gly	Arg	Arg	Asp		
545					550					555					560		
agc	ctg	cgc	aac	att	ctc	acc	att	tca	acc	gca	cca	aac	acc	aat	tgg	1728	
Ser	Leu	Arg	Asn	Ile	Leu	Thr	Ile	Ser	Thr	Ala	Pro	Asn	Thr	Asn	Trp		
			565						570					575			
tct	gag	gaa	gag	aag	aag	gaa	gag	atg	gac	aac	aac	tgc	cag	tcc	atc	1776	
Ser	Glu	Glu	Glu	Lys	Lys	Glu	Glu	Met	Asp	Asn	Asn	Cys	Gln	Ser	Ile		
			580					585					590				
ctc	gga	tac	gtt	gtg	cgc	tgg	gtt	gag	cac	ggt	gtt	ggt	tgc	tcc	aag	1824	
Leu	Gly	Tyr	Val	Val	Arg	Trp	Val	Glu	His	Gly	Val	Gly	Cys	Ser	Lys		
		595				600						605					
gtt	cca	gac	atc	cat	gac	atc	gac	ctc	atg	gaa	gac	cgc	gca	acg	ctg	1872	
Val	Pro	Asp	Ile	His	Asp	Ile	Asp	Leu	Met	Glu	Asp	Arg	Ala	Thr	Leu		
		610				615					620						
cgt	att	tcc	tcg	cag	atg	ctg	gcc	aac	tgg	atc	cgc	cat	gat	gtt	gtc	1920	
Arg	Ile	Ser	Ser	Gln	Met	Leu	Ala	Asn	Trp	Ile	Arg	His	Asp	Val	Val		

625	630	635	640	
tcg aag gag cag gtc ttg gag tca ctg gaa cga atg gca gtg gtc gtc				1968
Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val	645	650	655	
gac aag caa aat gcg ggc gac gag gcc tac cgc gat atg gcg ccg aag				2016
Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys	660	665	670	
tac gac gcc tcc ctc gcc ttc cag gcg gct aag gac ttg att ttc gaa				2064
Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu	675	680	685	
ggc acc aag tcc cca tcg ggc tac acc gag ccc atc ttg cac gca cgc				2112
Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg	690	695	700	
cgc cgc gag ttc aaa gca aaa aac taagcagcgt tttcgacgct tac				2159
Arg Arg Glu Phe Lys Ala Lys Asn	705	710		
<210> 596				
<211> 712				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 596				
Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu				
1 5 10 15				
Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala				
20 25 30				
Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg				
35 40 45				
Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly				
50 55 60				
Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr				
65 70 75 80				
Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp				
85 90 95				
Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu				
100 105 110				
Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu				
115 120 125				
Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala				
130 135 140				
Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu				
145 150 155 160				
Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser				
165 170 175				



His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala  
 180 185 190

His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg  
 195 200 205

Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr  
 210 215 220

Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly  
 225 230 235 240

Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile  
 245 250 255

Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu  
 260 265 270

Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu  
 275 280 285

Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu  
 290 295 300

Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu  
 305 310 315 320

His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln  
 325 330 335

Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met  
 340 345 350

Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln  
 355 360 365

Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro  
 370 375 380

Lys Gln His Gly Pro Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly  
 385 390 395 400

Arg Val Glu Asp Leu Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly  
 405 410 415

Val Met Asp Glu Glu Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile  
 420 425 430

Met Glu Val Ala Asp Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp  
 435 440 445

Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val  
 450 455 460

Arg Lys Ala Asp Met Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn  
 465 470 475 480

Asn Asn Val Asp Ala Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln  
 485 490 495

Ile Gly Lys Gly Met Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu  
                   500                                  505                                  510  
 Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val  
                   515                                  520                                  525  
 Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val  
                   530                                  535                                  540  
 Asp Val Phe Lys Val Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp  
                   545                                  550                                  555                                  560  
 Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp  
                                   565                                  570                                  575  
 Ser Glu Glu Glu Lys Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile  
                                   580                                  585                                  590  
 Leu Gly Tyr Val Val Arg Trp Val Glu His Gly Val Gly Cys Ser Lys  
                   595                                  600                                  605  
 Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu  
                   610                                  615                                  620  
 Arg Ile Ser Ser Gln Met Leu Ala Asn Trp Ile Arg His Asp Val Val  
                   625                                  630                                  635                                  640  
 Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val  
                                   645                                  650                                  655  
 Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys  
                                   660                                  665                                  670  
 Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu  
                   675                                  680                                  685  
 Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg  
                   690                                  695                                  700  
 Arg Arg Glu Phe Lys Ala Lys Asn  
                   705                                  710

&lt;210&gt; 597

&lt;211&gt; 873

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(850)

&lt;223&gt; RXA01089

&lt;400&gt; 597

aaaaattcgg ttcacaaaag gtttatcagt ccagcttaaa cccatcgac gggcgggaga 60

attagactca aggcacatca cattgaagga gcttcttattc ttg tct cga ttt gct 115  
   Leu Ser Arg Phe Ala  
   1                                  5

gcc aac ctg tca ttg act ttt act gag cta gat ttc ctg gat cgt ttt 163

Ala	Asn	Leu	Ser	Leu	Thr	Phe	Thr	Glu	Leu	Asp	Phe	Leu	Asp	Arg	Phe		
				10					15					20			
gat	gcc	gct	tcg	aag	cat	gct	ttc	agt	gcc	gtg	gag	ttt	cag	tac	cct	211	
Asp	Ala	Ala	Ser	Lys	His	Ala	Phe	Ser	Ala	Val	Glu	Phe	Gln	Tyr	Pro		
			25					30					35				
tac	gat	ttc	gat	gtt	caa	gag	att	aaa	cag	cgt	gct	gat	tcc	gca	ggt	259	
Tyr	Asp	Phe	Asp	Val	Gln	Glu	Ile	Lys	Gln	Arg	Ala	Asp	Ser	Ala	Gly		
		40					45					50					
ctg	ccc	att	gaa	ctg	ttc	aat	gcc	cca	cct	ggg	gat	act	ttt	ggt	ctt	307	
Leu	Pro	Ile	Glu	Leu	Phe	Asn	Ala	Pro	Pro	Gly	Asp	Thr	Phe	Gly	Leu		
	55					60					65						
gcg	gca	ctg	gct	tcc	cct	gaa	gac	ttt	caa	caa	tcc	atc	gag	cag	gcc	355	
Ala	Ala	Leu	Ala	Ser	Pro	Glu	Asp	Phe	Gln	Gln	Ser	Ile	Glu	Gln	Ala		
	70				75				80						85		
atc	acg	tac	gcc	aca	gtg	ttg	aag	cca	aag	aag	atg	cat	gtc	atg	gct	403	
Ile	Thr	Tyr	Ala	Thr	Val	Leu	Lys	Pro	Lys	Lys	Met	His	Val	Met	Ala		
				90				95						100			
ggc	atc	gcg	gac	gta	acc	tca	gaa	acc	acg	gcg	cgc	tat	gtg	gag	aat	451	
Gly	Ile	Ala	Asp	Val	Thr	Ser	Glu	Thr	Thr	Ala	Arg	Tyr	Val	Glu	Asn		
			105					110					115				
att	cgc	tgg	gct	gcg	cag	caa	cta	gac	aag	ctc	gac	gtt	gtc	gtt	gtt	499	
Ile	Arg	Trp	Ala	Ala	Gln	Gln	Leu	Asp	Lys	Leu	Asp	Val	Val	Val	Val		
		120					125					130					
att	gaa	cca	att	aat	cac	tat	tcg	gtt	ccc	ggt	tat	ttc	ctg	cac	act	547	
Ile	Glu	Pro	Ile	Asn	His	Tyr	Ser	Val	Pro	Gly	Tyr	Phe	Leu	His	Thr		
	135					140					145						
tta	gag	cag	gcg	tat	tgg	ctt	atc	gac	agc	att	gcc	cac	ccc	aat	gtg	595	
Leu	Glu	Gln	Ala	Tyr	Trp	Leu	Ile	Asp	Ser	Ile	Ala	His	Pro	Asn	Val		
	150				155					160					165		
aag	atc	tta	ttc	gat	act	ttc	cac	ctt	cag	cag	att	cat	ggc	aat	ctc	643	
Lys	Ile	Leu	Phe	Asp	Thr	Phe	His	Leu	Gln	Gln	Ile	His	Gly	Asn	Leu		
				170					175					180			
acc	cgc	cgc	ctg	cgc	gag	gtt	cat	ggc	gca	ggt	ctt	ttg	gga	cac	gtg	691	
Thr	Arg	Arg	Leu	Arg	Glu	Val	His	Gly	Ala	Gly	Leu	Leu	Gly	His	Val		
			185					190					195				
caa	gtg	gcc	tca	gtt	cct	gat	cga	cac	gaa	cct	ggc	act	ggc	gaa	gtc	739	
Gln	Val	Ala	Ser	Val	Pro	Asp	Arg	His	Glu	Pro	Gly	Thr	Gly	Glu	Val		
		200					205					210					
aat	gcg	gcg	tat	atc	ttc	caa	ctc	cta	agc	gaa	ctg	gga	tat	gac	ggt	787	
Asn	Ala	Ala	Tyr	Ile	Phe	Gln	Leu	Leu	Ser	Glu	Leu	Gly	Tyr	Asp	Gly		
	215					220					225						
gtc	atc	gct	ggc	gaa	tac	cac	cct	gct	ggt	gaa	act	aca	gcc	ggt	ttg	835	
Val	Ile	Ala	Gly	Glu	Tyr	His	Pro	Ala	Gly	Glu	Thr	Thr	Ala	Gly	Leu		
	230				235					240					245		
ggc	tgg	ttg	gag	ctc	tagatcgtaa	gtggtgtcgt	acc									873	
Gly	Trp	Leu	Glu	Leu													

250

<210> 598  
 <211> 250  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 598

```

Leu Ser Arg Phe Ala Ala Asn Leu Ser Leu Thr Phe Thr Glu Leu Asp
 1             5             10             15

Phe Leu Asp Arg Phe Asp Ala Ala Ser Lys His Ala Phe Ser Ala Val
      20             25             30

Glu Phe Gln Tyr Pro Tyr Asp Phe Asp Val Gln Glu Ile Lys Gln Arg
      35             40             45

Ala Asp Ser Ala Gly Leu Pro Ile Glu Leu Phe Asn Ala Pro Pro Gly
      50             55             60

Asp Thr Phe Gly Leu Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln
      65             70             75             80

Ser Ile Glu Gln Ala Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys
      85             90             95

Met His Val Met Ala Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala
      100            105            110

Arg Tyr Val Glu Asn Ile Arg Trp Ala Ala Gln Gln Leu Asp Lys Leu
      115            120            125

Asp Val Val Val Val Ile Glu Pro Ile Asn His Tyr Ser Val Pro Gly
      130            135            140

Tyr Phe Leu His Thr Leu Glu Gln Ala Tyr Trp Leu Ile Asp Ser Ile
      145            150            155            160

Ala His Pro Asn Val Lys Ile Leu Phe Asp Thr Phe His Leu Gln Gln
      165            170            175

Ile His Gly Asn Leu Thr Arg Arg Leu Arg Glu Val His Gly Ala Gly
      180            185            190

Leu Leu Gly His Val Gln Val Ala Ser Val Pro Asp Arg His Glu Pro
      195            200            205

Gly Thr Gly Glu Val Asn Ala Ala Tyr Ile Phe Gln Leu Leu Ser Glu
      210            215            220

Leu Gly Tyr Asp Gly Val Ile Ala Gly Glu Tyr His Pro Ala Gly Glu
      225            230            235            240

Thr Thr Ala Gly Leu Gly Trp Leu Glu Leu
      245            250

```

<210> 599  
 <211> 897  
 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(874)

&lt;223&gt; RXA01886

&lt;400&gt; 599

gcgaagctgc acgcaccgca ctactcatcg cactcggcgc catccgaagc gtagaaaccg 60

gcgcaaccat caaccttgct gaaagcatcg aggtttaacc atg act ttt aaa ctc 115  
 Met Thr Phe Lys Leu  
 1 5

gca gca tgc gca gag atg atc tac cag gac ctg cct ttc gag gag agg 163  
 Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu Pro Phe Glu Glu Arg  
 10 15 20

gtc aag acg atc tct gat cag gga ttc ctc gtg gaa att tgg gac tgg 211  
 Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val Glu Ile Trp Asp Trp  
 25 30 35

tcc aca aaa gac atc gat gcg ctc gtg gca aca ggc gcg gaa ttt tcc 259  
 Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr Gly Ala Glu Phe Ser  
 40 45 50

tcc atg acg ggc tac ctg cgc ggg gat ctg att act gaa cag ggc cgc 307  
 Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile Thr Glu Gln Gly Arg  
 55 60 65

gcg gag ctc ttg gca acc gct tcg gag tcc ttg gcg gtg gcg gaa aag 355  
 Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu Ala Val Ala Glu Lys  
 70 75 80 85

ctc aac tgc ccc cgg ctg aat ctg cat gga act ggc ctt gga ccg cag 403  
 Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr Gly Leu Gly Pro Gln  
 90 95 100

gga cta cct gtt act ccc att gaa gtg gtt acc cca gaa atg tgg ctc 451  
 Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr Pro Glu Met Trp Leu  
 105 110 115

tac gct gct gaa acg ctc cgc cag atc gct gag ctg ggg gag cgc gca 499  
 Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu Leu Gly Glu Arg Ala  
 120 125 130

ggc aag gtt ttc gtg ctg gaa aac ctc aac ctc gca gtc gat cac ccc 547  
 Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu Ala Val Asp His Pro  
 135 140 145

ggc act cct ttt gcc aag gcc act gac act ttg gcg ctg gtc aag gct 595  
 Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu Ala Leu Val Lys Ala  
 150 155 160 165

gtc aat cac ccg aat ctg cgc ctc aac ctg gat ttg tac cac gcc cag 643  
 Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp Leu Tyr His Ala Gln  
 170 175 180

att ggc gaa gga aac ctc att gag ctg ctc cgt gag gcg cag cca ttc 691  
 Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg Glu Ala Gln Pro Phe  
 185 190 195

atc ggc gaa atc cag gtt gcc gat gtc ccc ggc cgc atg gaa ccc ggc 739  
 Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly Arg Met Glu Pro Gly  
           200                                  205                                  210

acc ggc gag atc aac tac cag ggc gtc gcg aaa gct ctc gcc gcg atg 787  
 Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met  
           215                                  220                                  225

ggc tac gac ggc gtc atc ggc atg gag gcg tgg gca tcg ggc gac tcc 835  
 Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp Ala Ser Gly Asp Ser  
           230                                  235                                  240                                  245

agc gac gcg ctg cag gcg ttg aag tca gcg ttc acg gtc taaattgctt 884  
 Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe Thr Val  
                                   250                                  255

atcgacgcac ccc 897

<210> 600

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 600

Met Thr Phe Lys Leu Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu  
           1                                  5                                  10                                  15

Pro Phe Glu Glu Arg Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val  
                                   20                                  25                                  30

Glu Ile Trp Asp Trp Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr  
           35                                  40                                  45

Gly Ala Glu Phe Ser Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile  
           50                                  55                                  60

Thr Glu Gln Gly Arg Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu  
           65                                  70                                  75                                  80

Ala Val Ala Glu Lys Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr  
                                   85                                  90                                  95

Gly Leu Gly Pro Gln Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr  
           100                                  105                                  110

Pro Glu Met Trp Leu Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu  
           115                                  120                                  125

Leu Gly Glu Arg Ala Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu  
           130                                  135                                  140

Ala Val Asp His Pro Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu  
           145                                  150                                  155                                  160

Ala Leu Val Lys Ala Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp  
                                   165                                  170                                  175

Leu Tyr His Ala Gln Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg  
                                   180                                  185                                  190

Glu Ala Gln Pro Phe Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly  
 195 200 205

Arg Met Glu Pro Gly Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys  
 210 215 220

Ala Leu Ala Ala Met Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp  
 225 230 235 240

Ala Ser Gly Asp Ser Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe  
 245 250 255

Thr Val

<210> 601  
 <211> 1575  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (41)..(1552)  
 <223> RXN03117

<400> 601  
 tgtgcaacat tagttcgtta agaagagtca cattccagcc atg att acc cac gaa 55  
 Met Ile Thr His Glu  
 1 5

gtg cgc acc cac cgt tct gcg gaa gag ttc ccg tac aag aag cac ctg 103  
 Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu  
 10 15 20

gct cac aag atg gct cgc gtt gca gcc gac cca gtt gag gtt gct gcg 151  
 Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala  
 25 30 35

gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg 199  
 Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val  
 40 45 50

cag gca gct tcc gtg ttg cgt cga cca gtt agc tct gcc cgt gcg atg 247  
 Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met  
 55 60 65

gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt 295  
 Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly  
 70 75 80 85

ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act 343  
 Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr  
 90 95 100

gcg gtg cgt gag ctt gat ttc cat gac acg ttc ctc gct gcg gaa tac 391  
 Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr  
 105 110 115

tcc cac cca gga gat aac att cct ccg att ttg gct gca gca cag cag 439

Ser	His	Pro	Gly	Asp	Asn	Ile	Pro	Pro	Ile	Leu	Ala	Ala	Ala	Gln	Gln		
		120					125					130					
gct	gga	aaa	ggt	ggc	aag	gat	ctg	atc	cgt	ggc	atc	gct	act	ggg	tat	487	
Ala	Gly	Lys	Gly	Gly	Lys	Asp	Leu	Ile	Arg	Gly	Ile	Ala	Thr	Gly	Tyr		
	135					140				145							
gag	att	cag	gtt	aac	ttg	gtg	cgt	gga	atg	tgc	ctg	cat	gag	cac	aag	535	
Glu	Ile	Gln	Val	Asn	Leu	Val	Arg	Gly	Met	Cys	Leu	His	Glu	His	Lys		
150					155					160					165		
att	gat	cac	gtt	gct	cat	ctt	gga	cca	tca	gcg	gct	gct	ggt	atc	gga	583	
Ile	Asp	His	Val	Ala	His	Leu	Gly	Pro	Ser	Ala	Ala	Ala	Gly	Ile	Gly		
				170				175						180			
acc	ttg	cta	gac	cta	gat	gtg	gac	acc	atc	tac	cag	gca	att	ggt	cag	631	
Thr	Leu	Leu	Asp	Leu	Asp	Val	Asp	Thr	Ile	Tyr	Gln	Ala	Ile	Gly	Gln		
			185					190					195				
gca	ttg	cac	acc	acc	acg	gcg	acg	agg	cag	tcc	cgt	aaa	ggt	gcg	att	679	
Ala	Leu	His	Thr	Thr	Thr	Ala	Thr	Arg	Gln	Ser	Arg	Lys	Gly	Ala	Ile		
	200						205					210					
tct	tca	tgg	aag	gca	ttt	gct	cct	gcg	ttt	gcg	ggc	aag	atg	tcc	atc	727	
Ser	Ser	Trp	Lys	Ala	Phe	Ala	Pro	Ala	Phe	Ala	Gly	Lys	Met	Ser	Ile		
	215					220					225						
gag	gca	gta	gat	cgc	gca	atg	cgt	ggc	gag	ggc	gca	ccg	tca	cca	atc	775	
Glu	Ala	Val	Asp	Arg	Ala	Met	Arg	Gly	Glu	Gly	Ala	Pro	Ser	Pro	Ile		
230					235				240						245		
tgg	gaa	ggc	gaa	gac	ggc	gta	atc	gcg	tgg	ctg	ctg	tcc	ggt	ctt	gat	823	
Trp	Glu	Gly	Glu	Asp	Gly	Val	Ile	Ala	Trp	Leu	Leu	Ser	Gly	Leu	Asp		
				250					255					260			
cac	atc	tac	acc	att	cct	ttg	cct	gca	gaa	ggt	gaa	gcc	aaa	cga	gca	871	
His	Ile	Tyr	Thr	Ile	Pro	Leu	Pro	Ala	Glu	Gly	Glu	Ala	Lys	Arg	Ala		
			265					270					275				
atc	ttg	gat	acc	tac	acc	aag	gaa	cac	tcg	gcg	gaa	tac	cag	tca	cag	919	
Ile	Leu	Asp	Thr	Tyr	Thr	Lys	Glu	His	Ser	Ala	Glu	Tyr	Gln	Ser	Gln		
	280						285					290					
gca	ccg	atc	gac	ttg	gcg	cgc	agc	atg	ggg	gag	aag	ctg	gca	gca	cag	967	
Ala	Pro	Ile	Asp	Leu	Ala	Arg	Ser	Met	Gly	Glu	Lys	Leu	Ala	Ala	Gln		
	295					300					305						
ggc	ttg	gac	ctg	cgt	gat	gtg	gac	tcc	atc	gtt	ttg	cac	acc	tcc	cac	1015	
Gly	Leu	Asp	Leu	Arg	Asp	Val	Asp	Ser	Ile	Val	Leu	His	Thr	Ser	His		
310					315					320					325		
cac	act	cac	tac	gtg	atc	ggc	acc	gga	tct	aat	gat	cca	cag	aag	ttc	1063	
His	Thr	His	Tyr	Val	Ile	Gly	Thr	Gly	Ser	Asn	Asp	Pro	Gln	Lys	Phe		
				330				335						340			
gat	cca	gat	gca	tcg	cga	gaa	acc	ctt	gat	cac	tcc	atc	atg	tac	att	1111	
Asp	Pro	Asp	Ala	Ser	Arg	Glu	Thr	Leu	Asp	His	Ser	Ile	Met	Tyr	Ile		
			345					350					355				
ttc	gct	gtc	gcg	ctg	aag	gat	cgc	gcg	tgg	cac	cac	gag	cgt	tcc	tat	1159	
Phe	Ala	Val	Ala	Leu	Lys	Asp	Arg	Ala	Trp	His	His	Glu	Arg	Ser	Tyr		



360	365	370	
gct cct gag cga gcc cac cgc cga gag acc atc	gag ctg tgg aac aag	1207	
Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile	Glu Leu Trp Asn Lys		
375	380 385		
att tcc acg gtg gag gat cct gaa tgg acc agg	cgt tac cac tcc gtt	1255	
Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Val			
390	395 400 405		
gat cct gca gaa aag gcc ttc ggc gca cgc gca gtg atc acc ttc aag		1303	
Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala Val Ile Thr Phe Lys			
	410 415 420		
gat gga acc gtc gtg gaa gat gaa ctg gct gtg gcg aat gcg cat cct		1351	
Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val Ala Asn Ala His Pro			
	425 430 435		
ctg gga gca cgg cct ttc gct agg gag cag tac att cag aaa ttc cgc		1399	
Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr Ile Gln Lys Phe Arg			
	440 445 450		
acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa cag gat cgc ttc ttg		1447	
Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu Gln Asp Arg Phe Leu			
	455 460 465		
gat gcg gca cag cgt acg cac gag ctt gag gat ctt tca gaa ctc aac		1495	
Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp Leu Ser Glu Leu Asn			
	470 475 480 485		
att gaa ttg gat gcc gat att ttg gcc aag gct cct gtg att ccg gaa		1543	
Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala Pro Val Ile Pro Glu			
	490 495 500		
gga ctg ttc tgatggcggg tttgttttcc tct		1575	
Gly Leu Phe			

&lt;210&gt; 602

&lt;211&gt; 504

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 602

Met Ile Thr His Glu Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro	
1 5 10 15	
Tyr Lys Lys His Leu Ala His Lys Met Ala Arg Val Ala Ala Asp Pro	
20 25 30	
Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile	
35 40 45	
Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser	
50 55 60	
Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly	
65 70 75 80	
Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala	

85										90					95				
Leu	Ala	Asn	Gly	Thr	Ala	Val	Arg	Glu	Leu	Asp	Phe	His	Asp	Thr	Phe				
			100					105					110						
Leu	Ala	Ala	Glu	Tyr	Ser	His	Pro	Gly	Asp	Asn	Ile	Pro	Pro	Ile	Leu				
		115					120					125							
Ala	Ala	Ala	Gln	Gln	Ala	Gly	Lys	Gly	Gly	Lys	Asp	Leu	Ile	Arg	Gly				
		130				135					140								
Ile	Ala	Thr	Gly	Tyr	Glu	Ile	Gln	Val	Asn	Leu	Val	Arg	Gly	Met	Cys				
145					150					155					160				
Leu	His	Glu	His	Lys	Ile	Asp	His	Val	Ala	His	Leu	Gly	Pro	Ser	Ala				
				165					170					175					
Ala	Ala	Gly	Ile	Gly	Thr	Leu	Leu	Asp	Leu	Asp	Val	Asp	Thr	Ile	Tyr				
			180					185					190						
Gln	Ala	Ile	Gly	Gln	Ala	Leu	His	Thr	Thr	Thr	Ala	Thr	Arg	Gln	Ser				
		195					200					205							
Arg	Lys	Gly	Ala	Ile	Ser	Ser	Trp	Lys	Ala	Phe	Ala	Pro	Ala	Phe	Ala				
	210					215					220								
Gly	Lys	Met	Ser	Ile	Glu	Ala	Val	Asp	Arg	Ala	Met	Arg	Gly	Glu	Gly				
225					230					235					240				
Ala	Pro	Ser	Pro	Ile	Trp	Glu	Gly	Glu	Asp	Gly	Val	Ile	Ala	Trp	Leu				
				245					250					255					
Leu	Ser	Gly	Leu	Asp	His	Ile	Tyr	Thr	Ile	Pro	Leu	Pro	Ala	Glu	Gly				
			260					265					270						
Glu	Ala	Lys	Arg	Ala	Ile	Leu	Asp	Thr	Tyr	Thr	Lys	Glu	His	Ser	Ala				
		275					280					285							
Glu	Tyr	Gln	Ser	Gln	Ala	Pro	Ile	Asp	Leu	Ala	Arg	Ser	Met	Gly	Glu				
	290					295					300								
Lys	Leu	Ala	Ala	Gln	Gly	Leu	Asp	Leu	Arg	Asp	Val	Asp	Ser	Ile	Val				
305					310					315					320				
Leu	His	Thr	Ser	His	His	Thr	His	Tyr	Val	Ile	Gly	Thr	Gly	Ser	Asn				
				325					330					335					
Asp	Pro	Gln	Lys	Phe	Asp	Pro	Asp	Ala	Ser	Arg	Glu	Thr	Leu	Asp	His				
			340					345					350						
Ser	Ile	Met	Tyr	Ile	Phe	Ala	Val	Ala	Leu	Lys	Asp	Arg	Ala	Trp	His				
		355					360					365							
His	Glu	Arg	Ser	Tyr	Ala	Pro	Glu	Arg	Ala	His	Arg	Arg	Glu	Thr	Ile				
	370					375					380								
Glu	Leu	Trp	Asn	Lys	Ile	Ser	Thr	Val	Glu	Asp	Pro	Glu</							

Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val  
420 425 430

Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr  
435 440 445

Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu  
450 455 460

Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp  
465 470 475 480

Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala  
485 490 495

Pro Val Ile Pro Glu Gly Leu Phe  
500

<210> 603

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(975)

<223> FRXA00406

<400> 603

gac cca gtt gag gtt gct gcg gac act cag gaa atg atc atc acc cgc 48  
Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg  
1 5 10 15

atc atc gac aat gca tcg gtg cag gca gct tcc gtg ttg cgt cga cca 96  
Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro  
20 25 30

gtt agc tct gcc cgt gcg atg gca cag gtc agg cca gtt acc gat ggt 144  
Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly  
35 40 45

cgg ggt gca tct gtt ttc ggt ctg cca gga cgt tat gcc gcg gaa tgg 192  
Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp  
50 55 60

gct gcg ctt gct aac ggc act gcg gtg cgt gag ctt gat ttc cat gac 240  
Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp  
65 70 75 80

acg ttc ctc gct gcg gaa tac tcc cac cca gga gat aac att cct ccg 288  
Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro  
85 90 95

att ttg gct gca gca cag cag gct gga aaa ggt ggc aag gat ctg atc 336  
Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile  
100 105 110

cgt ggc atc gct act ggg tat gag att cag gtt aac ttg gtg cgt gga 384  
Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly

115	120	125	
atg tgc ctg cat gag cac aag att gat cac gtt gct cat ctt gga cca			432
Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro			
130	135	140	
tca gcg gct gct ggt atc gga acc ttg cta gac cta gat gtg gac acc			480
Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr			
145	150	155	160
atc tac cag gca att ggt cag gca ttg cac acc acc acg gcg acg agg			528
Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg			
	165	170	175
cag tcc cgt aaa ggt gcg att tct tca tgg aag gca ttt gct cct gcg			576
Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala			
	180	185	190
ttt gcg ggc aag atg tcc atc gag gca gta gat cgc gca atg cgt ggc			624
Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly			
	195	200	205
gag ggc gca ccg tca cca atc tgg gaa ggc gaa gac ggc gta atc gcg			672
Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala			
	210	215	220
tgg ctg ctg tcc ggt ctt gat cac atc tac acc att cct ttg cct gca			720
Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala			
225	230	235	240
gaa ggt gaa gcc aaa cga gca atc ttg gat acc tac acc aag gaa cac			768
Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His			
	245	250	255
tcg gcg gaa tac cag tca cag gca ccg atc gac ttg gcg cgc agc atg			816
Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met			
	260	265	270
ggg gag aag ctg gca gca cag ggc ttg gac ctg cgt gat gtg gac tcc			864
Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser			
	275	280	285
atc gtt ttg cac acc tcc cac cac act cac tac gtg atc ggc acc gga			912
Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly			
	290	295	300
tct aat gat cca cag aag ttc gat cca gat gca tcg cga gaa acc ctt			960
Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu			
305	310	315	320
gat cac tcc atc atg			975
Asp His Ser Ile Met			
	325		

&lt;210&gt; 604

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 604

Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg  
 1 5 10 15  
 Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro  
 20 25 30  
 Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly  
 35 40 45  
 Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp  
 50 55 60  
 Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp  
 65 70 75 80  
 Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro  
 85 90 95  
 Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile  
 100 105 110  
 Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly  
 115 120 125  
 Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro  
 130 135 140  
 Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr  
 145 150 155 160  
 Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg  
 165 170 175  
 Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala  
 180 185 190  
 Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly  
 195 200 205  
 Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala  
 210 215 220  
 Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala  
 225 230 235 240  
 Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His  
 245 250 255  
 Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met  
 260 265 270  
 Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser  
 275 280 285  
 Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly  
 290 295 300  
 Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu  
 305 310 315 320  
 Asp His Ser Ile Met

325

<210> 605  
 <211> 431  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(408)  
 <223> FRXA00514

<400> 605  
 cac gag cgt tcc tat gct cct gag cga gcc ctc cgc cga gag acc atc 48  
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile  
 1 5 10 15  
 gag ctg tgg aac aag att tcc acg gtg gag gat cct gaa tgg acc agg 96  
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg  
 20 25 30  
 cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca 144  
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala  
 35 40 45  
 gtg atc acc ttc aag gat gga acc gtc gtg gaa gat gaa ctg gct gtg 192  
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val  
 50 55 60  
 gcg aat gcg cat cct ctg gga gca cgg cct ttc gct agg gag cag tac 240  
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr  
 65 70 75 80  
 att cag aaa ttc cgc acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa 288  
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu  
 85 90 95  
 cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat 336  
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp  
 100 105 110  
 ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct 384  
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala  
 115 120 125  
 cct gtg att ccg gaa gga ctg ttc tgatggcggg tttgttttcc tct 431  
 Pro Val Ile Pro Glu Gly Leu Phe  
 130 135

<210> 606  
 <211> 136  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 606  
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile  
 1 5 10 15  
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg

20 25 30  
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala  
 35 40 45  
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val  
 50 55 60  
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr  
 65 70 75 80  
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu  
 85 90 95  
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp  
 100 105 110  
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala  
 115 120 125  
 Pro Val Ile Pro Glu Gly Leu Phe  
 130 135

<210> 607  
 <211> 718  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(718)  
 <223> RXA00512

<400> 607  
 tacaacgagt acaacgcttt cgaccagcaa gtattcacct attccgctga cagctacaag 60  
 cccatcttct aaccgccta tatataagga gtgaatcacc atg tcc agc gcc aca 115  
 Met Ser Ser Ala Thr  
 1 5  
 acc act gat gtt cgc aaa ggg ctc tac gga gtc atc gcc gat tac acg 163  
 Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val Ile Ala Asp Tyr Thr  
 10 15 20  
 gcc gtt tcc aaa gtc atg cca gag acc aat tca ctg acc tac cgt ggc 211  
 Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser Leu Thr Tyr Arg Gly  
 25 30 35  
 tac gcg gtg gaa gat ttg gtg gaa aac tgc agc ttc gag gag gtg ttt 259  
 Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Phe  
 40 45 50  
 tac ctc ctg tgg cac ggc gag ctg ccc act gcg caa caa ctt gcg gag 307  
 Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala Gln Gln Leu Ala Glu  
 55 60 65  
 ttc aat gag cgt ggc cgt tcc tac cgc tcc ctg gat gcc ggt ttg atc 355  
 Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile  
 70 75 80 85

tcc ctg atc cac tct ttg ccc aaa gaa gcc cac ccg atg gat gtt atg 403  
 Ser Leu Ile His Ser Leu Pro Lys Glu Ala His Pro Met Asp Val Met  
 90 95 100

cgc acc gcg gtg tcc tac atg ggc acc aag gat tcc gag tat ttc acc 451  
 Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp Ser Glu Tyr Phe Thr  
 105 110 115

acc gat tct gag cac atc cgc aaa gtt ggc cac acc ttg ttg gcg cag 499  
 Thr Asp Ser Glu His Ile Arg Lys Val Gly His Thr Leu Leu Ala Gln  
 120 125 130

ctt ccg atg gtg cta gcc atg gat att cgt cgc cgc aag ggc ctc gat 547  
 Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg Arg Lys Gly Leu Asp  
 135 140 145

atc atc gcc cct gac tcc agc aag tca gtc gcc gaa aac ctg ctg tct 595  
 Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala Glu Asn Leu Leu Ser  
 150 155 160 165

atg gtg ttt ggt act ggc ccg gaa tca cct gca tcc aac cca gct gac 643  
 Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala Ser Asn Pro Ala Asp  
 170 175 180

gtc cgc gat ttt gag aaa tca ctg atc ctc tac gcc gag cac tcc ttc 691  
 Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr Ala Glu His Ser Phe  
 185 190 195

aac gcc tcc acc ttc acc gcc cgc gtg 718  
 Asn Ala Ser Thr Phe Thr Ala Arg Val  
 200 205

<210> 608  
 <211> 206  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 608  
 Met Ser Ser Ala Thr Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val  
 1 5 10 15  
 Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser  
 20 25 30  
 Leu Thr Tyr Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser  
 35 40 45  
 Phe Glu Glu Val Phe Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala  
 50 55 60  
 Gln Gln Leu Ala Glu Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu  
 65 70 75 80  
 Asp Ala Gly Leu Ile Ser Leu Ile His Ser Leu Pro Lys Glu Ala His  
 85 90 95  
 Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp  
 100 105 110  
 Ser Glu Tyr Phe Thr Thr Asp Ser Glu His Ile Arg Lys Val Gly His



115	120	125
Thr Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg 130 135 140		
Arg Lys Gly Leu Asp Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala 145 150 155 160		
Glu Asn Leu Leu Ser Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala 165 170 175		
Ser Asn Pro Ala Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr 180 185 190		
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ala Arg Val 195 200 205		

&lt;210&gt; 609

&lt;211&gt; 320

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(297)

&lt;223&gt; RXA00518

&lt;400&gt; 609

gtc ctt ccg gta tta gct gcc cgc cac gac ggc gaa aag tgg gtt gcc Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala 1 5 10 15	48
atg tat gaa aac atg cgc gac gcc atg gac gcc cgc acc ggc atc aag Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys 20 25 30	96
ccg aat ctc gat ttc cct gct ggc cct gcc tac cac ctg ctc ggt ttc Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe 35 40 45	144
ccg gtc gat ttc ttc acc ccg ctg ttc gtc atc gcc cgc gtc gcc ggc Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly 50 55 60	192
tgg acg gcc cac atc gtg gag cag tac gaa aac aac tcg ctc atc cgc Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg 65 70 75 80	240
cca ctg tcc gag tac aac ggc gag gag cag cgc gag gtc gcg ccc att Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile 85 90 95	288
gaa aag cgc taaaagattt tcgcttttcg acg Glu Lys Arg	320

&lt;210&gt; 610

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 610

Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala  
 1 5 10 15

Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys  
 20 25 30

Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe  
 35 40 45

Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly  
 50 55 60

Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg  
 65 70 75 80

Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile  
 85 90 95

Glu Lys Arg

&lt;210&gt; 611

&lt;211&gt; 1494

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1471)

&lt;223&gt; RXA01077

&lt;400&gt; 611

tctatgactt gatccacaat gtgatgcaaa tcattgaccc tcaccccgga ccaagcgctt 60

aatgaaggca agccaaactt aactagtaga taggattgca atg acc gaa tcg caa 115  
 Met Thr Glu Ser Gln  
 1 5

gat ctc gcc gca ttc gtg gaa gct gcc aaa ctc aat gat gca agc ccc 163  
 Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu Asn Asp Ala Ser Pro  
 10 15 20

gaa gcc gta gag caa ttg aaa atc aga gtg cta gac acc gta ggc gtt 211  
 Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu Asp Thr Val Gly Val  
 25 30 35

gcc att ggc gca ctg gat gcc gaa ccg att gtc gcc att cga gga ctc 259  
 Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val Ala Ile Arg Gly Leu  
 40 45 50

ctg gaa gac ctc ggg gga acc gaa cag tca aca ctt att ggt ggt ggc 307  
 Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr Leu Ile Gly Gly Gly  
 55 60 65

aaa acc agt ccg gaa cgt gca gca ttt ttc aac agc gca tta agc cgc 355  
 Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn Ser Ala Leu Ser Arg  
 70 75 80 85

tac ctc gac ttc atg gac gcc tac cta gca aag ggc gaa acc aac cac	403
Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys Gly Glu Thr Asn His	
90 95 100	
ccc tcg gat aac ttc gga gca gtg ctc gct gca gcc gaa agc gtt ggc	451
Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala Ala Glu Ser Val Gly	
105 110 115	
gcc tct gga aaa gac ctg ctc acc gca ttc gcc gtg gcc tac cag gta	499
Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala Val Ala Tyr Gln Val	
120 125 130	
cac acc aga ctt tca gat gtc gca cca gtt cgc gcc aaa ggt ttc gat	547
His Thr Arg Leu Ser Asp Val Ala Pro Val Arg Ala Lys Gly Phe Asp	
135 140 145	
cac acc acc caa gga gca ttc gca gcg ggc gca tct gct gcc aag gca	595
His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala Ser Ala Ala Lys Ala	
150 155 160 165	
ctg ggt ttg cca gct gat caa atc gcc aac gca ctg gcc atc gca gga	643
Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala Leu Ala Ile Ala Gly	
170 175 180	
aca gcc aat gtt gca ctt cgt gtc act cgc act gga aac ttg agc cac	691
Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr Gly Asn Leu Ser His	
185 190 195	
tgg aaa ggc ctt gcc tac cca cac gtg tcc aaa gaa gga acc tgg gca	739
Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys Glu Gly Thr Trp Ala	
200 205 210	
gca ctg ctc gca agc cga ggt att acc ggt ccg gaa gaa gtc ttc gaa	787
Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro Glu Glu Val Phe Glu	
215 220 225	
ggc aac aag gga ttc aaa gag tcc gtc tcc gga ccg ttc gag atc gat	835
Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly Pro Phe Glu Ile Asp	
230 235 240 245	
tgg tcc aag gaa gac ttg gaa agc gtt aag cgc acc atc atc aag aaa	883
Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg Thr Ile Ile Lys Lys	
250 255 260	
cac aac gcg gaa att cac tcg cag tca gcg ctt gat gca gcc caa gaa	931
His Asn Ala Glu Ile His Ser Gln Ser Ala Leu Asp Ala Ala Gln Glu	
265 270 275	
ata cgc gca caa gaa ggc ttc aat gtg gac aac att gaa aag att cac	979
Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn Ile Glu Lys Ile His	
280 285 290	
ctg act act ttc gac gtt gcc tac tcc atc att ggc ggc ggc gaa gaa	1027
Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile Gly Gly Gly Glu Glu	
295 300 305	
ggc gac aaa cag ctt att cgc acc aaa gaa gaa gcc gat cac tca ctg	1075
Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu Ala Asp His Ser Leu	
310 315 320 325	

ccg tgg atg ctc gct gta gtt ctg ctg gat ggt cag ctc aat ccc gaa 1123  
 Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly Gln Leu Asn Pro Glu  
 330 335 340

cag tac gaa cca tca cgc atc gtt gct gat gat gta caa acc ttg atg 1171  
 Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp Val Gln Thr Leu Met  
 345 350 355

aag aaa atc gaa atc aca ccg tca gat gaa ttc tct gat cgc ttc cct 1219  
 Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe Ser Asp Arg Phe Pro  
 360 365 370

gac cac atg cca gct gat cta gaa gtc aca cta aac gat ggc tcg gtg 1267  
 Asp His Met Pro Ala Asp Leu Glu Val Thr Leu Asn Asp Gly Ser Val  
 375 380 385

ttc aaa gct tca caa gat agc tac tta ggc ttc cac gac aat ccc cta 1315  
 Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe His Asp Asn Pro Leu  
 390 395 400 405

gat tgg gac aac gcg cgc aag aaa ttc gat gcc ctt gtc aca cca ttc 1363  
 Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala Leu Val Thr Pro Phe  
 410 415 420

acc ggt gaa gaa cta cgt gaa gaa atc gcc acg atc att cac gag ctc 1411  
 Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr Ile Ile His Glu Leu  
 425 430 435

gat agc cga cag gtt tct gaa ctc aca gaa gcc ctg gcc aaa gtc tcc 1459  
 Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala Leu Ala Lys Val Ser  
 440 445 450

acc acc cgc agc taaaactttt tgaaaggagc tca 1494  
 Thr Thr Arg Ser  
 455

&lt;210&gt; 612

&lt;211&gt; 457

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 612

Met Thr Glu Ser Gln Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu  
 1 5 10 15

Asn Asp Ala Ser Pro Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu  
 20 25 30

Asp Thr Val Gly Val Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val  
 35 40 45

Ala Ile Arg Gly Leu Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr  
 50 55 60

Leu Ile Gly Gly Gly Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn  
 65 70 75 80

Ser Ala Leu Ser Arg Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys  
 85 90 95

Gly Glu Thr Asn His Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala  
 100 105 110  
 Ala Glu Ser Val Gly Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala  
 115 120 125  
 Val Ala Tyr Gln Val His Thr Arg Leu Ser Asp Val Ala Pro Val Arg  
 130 135 140  
 Ala Lys Gly Phe Asp His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala  
 145 150 155 160  
 Ser Ala Ala Lys Ala Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala  
 165 170 175  
 Leu Ala Ile Ala Gly Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr  
 180 185 190  
 Gly Asn Leu Ser His Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys  
 195 200 205  
 Glu Gly Thr Trp Ala Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro  
 210 215 220  
 Glu Glu Val Phe Glu Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly  
 225 230 235 240  
 Pro Phe Glu Ile Asp Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg  
 245 250 255  
 Thr Ile Ile Lys Lys His Asn Ala Glu Ile His Ser Gln Ser Ala Leu  
 260 265 270  
 Asp Ala Ala Gln Glu Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn  
 275 280 285  
 Ile Glu Lys Ile His Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile  
 290 295 300  
 Gly Gly Gly Glu Glu Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu  
 305 310 315 320  
 Ala Asp His Ser Leu Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly  
 325 330 335  
 Gln Leu Asn Pro Glu Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp  
 340 345 350  
 Val Gln Thr Leu Met Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe  
 355 360 365  
 Ser Asp Arg Phe Pro Asp His Met Pro Ala Asp Leu Glu Val Thr Leu  
 370 375 380  
 Asn Asp Gly Ser Val Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe  
 385 390 395 400  
 His Asp Asn Pro Leu Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala  
 405 410 415  
 Leu Val Thr Pro Phe Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr

420

425

430

Ile Ile His Glu Leu Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala  
 435 440 445

Leu Ala Lys Val Ser Thr Thr Arg Ser  
 450 455

&lt;210&gt; 613

&lt;211&gt; 923

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(900)

&lt;223&gt; RXN03144

&lt;400&gt; 613

acc acg acg gct acc agg cag tcg cga aaa ggt gag att tcc agc tgg 48  
 Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp  
 1 5 10 15

aag gcg ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg 96  
 Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met  
 20 25 30

gat cgt gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc 144  
 Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly  
 35 40 45

gaa gac ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat 192  
 Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr  
 50 55 60

cat gtg cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag 240  
 His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu  
 65 70 75 80

act tac aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att 288  
 Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile  
 85 90 95

gat ctg gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg 336  
 Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr  
 100 105 110

gaa cac att gca gag att gtg ctg cgc acc agt cac cac acg cat tat 384  
 Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr  
 115 120 125

gtg att ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc 432  
 Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala  
 130 135 140

tcg cgt gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg 480  
 Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala  
 145 150 155 160

ctt caa gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt 528

Leu	Gln	Asp	Gly	Val	Trp	His	His	Glu	Phe	Ser	Tyr	Thr	Arg	Lys	Arg		
				165					170					175			
tcc	acc	cgc	ccg	gaa	act	gtg	gag	ctg	tgg	cac	aag	att	cgc	acc	gtg	576	
Ser	Thr	Arg	Pro	Glu	Thr	Val	Glu	Leu	Trp	His	Lys	Ile	Arg	Thr	Val		
				180					185					190			
gag	gat	cct	gaa	tgg	acg	cgc	cga	tac	cat	tct	gat	gat	cct	gca	aaa	624	
Glu	Asp	Pro	Glu	Trp	Thr	Arg	Arg	Tyr	His	Ser	Asp	Asp	Pro	Ala	Lys		
				195					200					205			
aag	gcc	ttt	ggt	gcg	aaa	gca	gtg	atc	aca	atg	gct	gat	ggc	acc	gtg	672	
Lys	Ala	Phe	Gly	Ala	Lys	Ala	Val	Ile	Thr	Met	Ala	Asp	Gly	Thr	Val		
				210					215					220			
att	gag	gat	gaa	ttg	gct	gtc	gcg	gat	gcc	cac	ccg	ctg	ggg	gct	cgg	720	
Ile	Glu	Asp	Glu	Leu	Ala	Val	Ala	Asp	Ala	His	Pro	Leu	Gly	Ala	Arg		
				225					230					235			240
ccg	ttt	gcg	cgg	gag	aat	tac	att	gaa	aaa	ttc	cgc	aca	ctc	gcg	cag	768	
Pro	Phe	Ala	Arg	Glu	Asn	Tyr	Ile	Glu	Lys	Phe	Arg	Thr	Leu	Ala	Gln		
				245					250					255			
ggg	att	gtc	att	gat	tca	gaa	cag	gaa	cgc	ttc	ttg	cat	gcc	gtg	caa	816	
Gly	Ile	Val	Ile	Asp	Ser	Glu	Gln	Glu	Arg	Phe	Leu	His	Ala	Val	Gln		
				260					265					270			
agc	ctg	cct	gac	ctg	gat	gat	ctt	gat	cag	ctc	aac	atc	gaa	gtc	gac	864	
Ser	Leu	Pro	Asp	Leu	Asp	Asp	Leu	Asp	Gln	Leu	Asn	Ile	Glu	Val	Asp		
				275					280					285			
ata	agc	aac	cag	gcc	gcg	acg	aaa	gcg	ggg	ctg	tta	tga	atc	tct	tct	910	
Ile	Ser	Asn	Gln	Ala	Ala	Thr	Lys	Ala	Gly	Leu	Leu						
				290					295					300			
ttcgaatggt gtt																923	

<210> 614

$\langle 211 \rangle$  300

<212> PRT

<213> Corynebacterium glutamicum

<400> 614

Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp  
1 5 10 15

Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met  
20 25 30

Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly  
35 40 45

Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr  
50 55 60

His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu  
65 70 75 80

Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile  
85 90 95

Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr  
 100 105 110  
 Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr  
 115 120 125  
 Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala  
 130 135 140  
 Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala  
 145 150 155 160  
 Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg  
 165 170 175  
 Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val  
 180 185 190  
 Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys  
 195 200 205  
 Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val  
 210 215 220  
 Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg  
 225 230 235 240  
 Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln  
 245 250 255  
 Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln  
 260 265 270  
 Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp  
 275 280 285  
 Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu  
 290 295 300

<210> 615  
 <211> 511  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(511)  
 <223> FRXA02322

<400> 615  
 cgcgcagagc taaactgcgt gaggttgtgg cctgtcacac ataatcggcc taggggtggga 60  
 cttaaggaa acagtgcaca aataaatctc aaggagcccc atg cgc.atc cac gat 115  
 Met Arg Ile His Asp  
 1 5  
 gtt tat acc cac ctt tcg gcc gat aac ttt ccc aaa gca gag cac ctt 163  
 Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro Lys Ala Glu His Leu  
 10 15 20



gcg tgg aaa ttc tcc gag ctt gcc acc gac ccc gtg gag gtg aca ccg 211  
 Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro Val Glu Val Thr Pro  
                   25                                  30                                  35

gat gtt tcg gag atg atc atc aac cgg atc atc gac aac gcg gcg gtg 259  
 Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile Asp Asn Ala Ala Val  
                   40                                  45                                  50

tct gcc gcg tcg gtg ttg cgc cgg cct gtg act gtg gcc agg caa caa 307  
 Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr Val Ala Arg Gln Gln  
                   55                                  60                                  65

gcg cag tcc cat ccg cgg gaa aag ggc gga aaa gtt ttt gga att tca 355  
 Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys Val Phe Gly Ile Ser  
                   70                                  75                                  80                                  85

ggc agc tac tca cca gag tgg gct gcc ttt gct aat ggt gtg gcc gta 403  
 Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala Asn Gly Val Ala Val  
                                   90                                  95                                  100

cgt gaa ttg gac ttc cac gat aca ttt tta gca gct gaa tac tcc cat 451  
 Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr Ser His  
                                   105                                  110                                  115

ccc ggc gac aat att cca cca ctt ctt gca gta gcg cag gct cag aga 499  
 Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val Ala Gln Ala Gln Arg  
                   120                                  125                                  130

agc agc ggc agg 511  
 Ser Ser Gly Arg  
                   135

&lt;210&gt; 616

&lt;211&gt; 137

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 616

Met Arg Ile His Asp Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro  
   1                                  5                                  10                                  15

Lys Ala Glu His Leu Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro  
                   20                                  25                                  30

Val Glu Val Thr Pro Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile  
                   35                                  40                                  45

Asp Asn Ala Ala Val Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr  
                   50                                  55                                  60

Val Ala Arg Gln Gln Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys  
                   65                                  70                                  75                                  80

Val Phe Gly Ile Ser Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala  
                                   85                                  90                                  95

Asn Gly Val Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala  
                   100                                  105                                  110

Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val  
 115 120 125

Ala Gln Ala Gln Arg Ser Ser Gly Arg  
 130 135

<210> 617

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(603)

<223> RXA02329

<400> 617

acg gct acc agg cag tcg cga aaa ggt gag att tcc agc tgg aag gcg 48  
 Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala  
 1 5 10 15

ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg gat cgt 96  
 Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg  
 20 25 30

gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc gaa gac 144  
 Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp  
 35 40 45

ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat cat gtg 192  
 Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val  
 50 55 60

cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag act tac 240  
 Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr  
 65 70 75 80

aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att gat ctg 288  
 Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu  
 85 90 95

gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg gaa cac 336  
 Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His  
 100 105 110

att gca gag att gtg ctg cgc acc agt cac cac acg cat tat gtg att 384  
 Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile  
 115 120 125

ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc tcg cgt 432  
 Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg  
 130 135 140

gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg ctt caa 480  
 Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln  
 145 150 155 160

gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt tcc acc 528  
 Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr  
 165 170 175

cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg gag gat 576  
 Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp  
                   180                                  190

cct gaa tgg acg cgc cga tac cat tct 603  
 Pro Glu Trp Thr Arg Arg Tyr His Ser  
                   195                                  200

<210> 618

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 618

Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala  
   1                                  5                                  10                                  15

Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg  
                   20                                  25                                  30

Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp  
                   35                                  40                                  45

Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val  
                   50                                  55                                  60

Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr  
                   65                                  70                                  75                                  80

Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu  
                                   85                                  90                                  95

Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His  
                   100                                  105                                  110

Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile  
                   115                                  120                                  125

Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg  
                   130                                  135                                  140

Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln  
                   145                                  150                                  155                                  160

Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr  
                                   165                                  170                                  175

Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp  
                   180                                  185                                  190

Pro Glu Trp Thr Arg Arg Tyr His Ser  
                   195                                  200

<210> 619

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1243)  
 <223> RXA02332

<400> 619

```

gaccgcatgc aacaccgcag cagattatat gagctcctgc gatacgaaga ctacaacgtc 60

tttgaccagc acattttcac ctacagaaaa ggagaaaaaca atg agt gac agc caa 115
                                   Met Ser Asp Ser Gln
                                   1 5

gtc cgc aaa gga ctc aac ggc gtc atc tct gac tac aca agc att tcc 163
Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp Tyr Thr Ser Ile Ser
              10              15              20

aaa gtg atg cca gag agc aac tcg ctg act tac cgt ggc tac gcc gtg 211
Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr Arg Gly Tyr Ala Val
              25              30              35

gag gat ttg gtg gaa aac tgc agc ttt gaa gaa gtg atc tac ctc ctg 259
Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Ile Tyr Leu Leu
              40              45              50

tgg ttt ggg gag ctg ccc acc act gaa caa ctc cgg acc ttc aac acg 307
Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu Arg Thr Phe Asn Thr
              55              60              65

aca ggt cga agc tac cgc tca ctc gac gcc gga ctg att tcc ctc atc 355
Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile Ser Leu Ile
              70              75              80              85

cac tcc tta ccc aac acc tgc cac ccc atg gac gtg ctg cgc acc gca 403
His Ser Leu Pro Asn Thr Cys His Pro Met Asp Val Leu Arg Thr Ala
              90              95              100

gtg tcc tac atg ggt acc ttt gat ccc gat ccg ttt acc cgc gat gcc 451
Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro Phe Thr Arg Asp Ala
              105              110              115

gat cat atc cga agc att gga cac aac ctg ctt gcg cag ctt ccc atg 499
Asp His Ile Arg Ser Ile Gly His Asn Leu Leu Ala Gln Leu Pro Met
              120              125              130

gtg gtt gcc atg gat atc cgc agg cga agt ggg gaa gag atc atc gca 547
Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly Glu Glu Ile Ile Ala
              135              140              145

cct gac cac aac aaa ggt atc gct tcg aat ttc tta tcc atg gtg ttt 595
Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe Leu Ser Met Val Phe
              150              155              160              165

ggc aat gat gat ggt tct gta gcc aac tcc gca gat gac atc cgc gat 643
Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala Asp Asp Ile Arg Asp
              170              175              180

ttt gaa cgc tcc ctc atc ctc tac gcc gag cac tcc ttc aac gcc tcc 691
Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His Ser Phe Asn Ala Ser
              185              190              195

aca ttc tca gcc cgc gtg atc tca tca acg cga tcc gat acg tat tcg 739

```

Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg Ser Asp Thr Tyr Ser  
 200 205 210  
 gcg atc aca ggt gcg atc ggt gct ctc aaa ggc cca ctg cac gga ggt 787  
 Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Leu His Gly Gly  
 215 220 225  
 gcc aat gag ttt gtc atg cac acc atg ctg gat atc gac gat ccc aac 835  
 Ala Asn Glu Phe Val Met His Thr Met Leu Asp Ile Asp Asp Pro Asn  
 230 235 240 245  
 aat gct gcc gac tgg atg ggc aag gcg ttg gat cgt aaa gaa cgc atc 883  
 Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp Arg Lys Glu Arg Ile  
 250 255 260  
 atg gga ttc ggg cac cgc gtg tac aaa aac ggc gac tcc agg gtc ccc 931  
 Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly Asp Ser Arg Val Pro  
 265 270 275  
 tcc atg gag aaa tcc atg cgc tcc ctt gct gct cgt cac cgt ggt caa 979  
 Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala Arg His Arg Gly Gln  
 280 285 290  
 aaa tgg gtg cac atg tat gag tcg atg caa gaa gtc atg gag gct cgc 1027  
 Lys Trp Val His Met Tyr Glu Ser Met Gln Glu Val Met Glu Ala Arg  
 295 300 305  
 act ggc att aaa ccc aac ctc gac ttc ccg gcc ggc cct gcc tat tac 1075  
 Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr Tyr  
 310 315 320 325  
 atg ctg gga ttc ccc gtc gac ttc ttc aca cca ctg ttt gtg ctg gcc 1123  
 Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro Leu Phe Val Leu Ala  
 330 335 340  
 cga gtg tca ggg tgg acg gca cac atc gtg gag caa ttt gaa aac aat 1171  
 Arg Val Ser Gly Trp Thr Ala His Ile Val Glu Gln Phe Glu Asn Asn  
 345 350 355  
 gcg ctg atc cga cca ttg tct gcc tac aac gga gtg gaa gaa agg gag 1219  
 Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly Val Glu Glu Arg Glu  
 360 365 370  
 gtg gtg ccc att tcg gag aga acc taatcagtga ggctgatttc taa 1266  
 Val Val Pro Ile Ser Glu Arg Thr  
 375 380

&lt;210&gt; 620

&lt;211&gt; 381

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 620

Met Ser Asp Ser Gln Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp  
 1 5 10 15

Tyr Thr Ser Ile Ser Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr  
 20 25 30

Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu

35	40	45
Val Ile Tyr Leu Leu Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu		
50	55	60
Arg Thr Phe Asn Thr Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly		
65	70	75
Leu Ile Ser Leu Ile His Ser Leu Pro Asn Thr Cys His Pro Met Asp		
85	90	95
Val Leu Arg Thr Ala Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro		
100	105	110
Phe Thr Arg Asp Ala Asp His Ile Arg Ser Ile Gly His Asn Leu Leu		
115	120	125
Ala Gln Leu Pro Met Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly		
130	135	140
Glu Glu Ile Ile Ala Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe		
145	150	155
Leu Ser Met Val Phe Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala		
165	170	175
Asp Asp Ile Arg Asp Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His		
180	185	190
Ser Phe Asn Ala Ser Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg		
195	200	205
Ser Asp Thr Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly		
210	215	220
Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr Met Leu Asp		
225	230	235
Ile Asp Asp Pro Asn Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp		
245	250	255
Arg Lys Glu Arg Ile Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly		
260	265	270
Asp Ser Arg Val Pro Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala		
275	280	285
Arg His Arg Gly Gln Lys Trp Val His Met Tyr Glu Ser Met Gln Glu		
290	295	300
Val Met Glu Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala		
305	310	315
Gly Pro Ala Tyr Tyr Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro		
325	330	335
Leu Phe Val Leu Ala Arg Val Ser Gly Trp Thr Ala His Ile Val Glu		
340	345	350
Gln Phe Glu Asn Asn Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly		
355	360	365

Val Glu Glu Arg Glu Val Val Pro Ile Ser Glu Arg Thr  
 370 375 380

<210> 621  
 <211> 1038  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1015)  
 <223> RXN02333

<400> 621  
 tcttgcatgc cgtgcaaagc ctgcctgacc tggatgatct tgatcagctc aacatcgaag 60  
 tcgacataag caaccaggcc gcgacgaaag cggggctgtt atg aat ctc ttt tcg 115  
 Met Asn Leu Phe Ser  
 1 5  
 aat ggt gtt gat gtg ggg agg cgt cga caa gca ttt aaa gcg gca ctc 163  
 Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala Phe Lys Ala Ala Leu  
 10 15 20  
 gcc gca ccc cac atc gcc cgg ctg ccc ggc gca ttc tcc cct ctg att 211  
 Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala Phe Ser Pro Leu Ile  
 25 30 35  
 gcg cgc tcc atc gaa gaa gcc ggc ttc gaa ggc gtc tac gtt tcc ggc 259  
 Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly Val Tyr Val Ser Gly  
 40 45 50  
 gcc gtc ata gct gct gac ctg gca cta ccc gat atc ggc ttg acg acg 307  
 Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp Ile Gly Leu Thr Thr  
 55 60 65  
 ctg acc gaa gtc gcc cac cgc gcg cgg caa att gcg cgc gtc aca gac 355  
 Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile Ala Arg Val Thr Asp  
 70 75 80 85  
 cta gga gtg ctt gtc gac gcc gac acc ggc ttt ggc gaa ccc atg tcg 403  
 Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe Gly Glu Pro Met Ser  
 90 95 100  
 gcc gca cgc acc gtc gcc gaa ttg gag gac gcc ggt gtg gcc gga tgc 451  
 Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala Gly Val Ala Gly Cys  
 105 110 115  
 cac ctt gaa gac caa gtc aac ccc aaa cgt tgc ggc cac ttg gac ggc 499  
 His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys Gly His Leu Asp Gly  
 120 125 130  
 aaa gaa gtc gtg cgc aca gac gtg atg gtt cga cgc atc gca gcc gcc 547  
 Lys Glu Val Val Arg Thr Asp Val Met Val Arg Arg Ile Ala Ala Ala  
 135 140 145  
 gtc tcg gcc cgg cgc gac ccg aac ttt gtc atc tgc gcc cgc acc gac 595  
 Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile Cys Ala Arg Thr Asp  
 150 155 160 165

gcc gct gga gtg gaa gga atc gac gcc gcc att gag cgc gcg aaa gcc 643  
 Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile Glu Arg Ala Lys Ala  
 170 175 180

tac tta gat gcg ggc gcc gac atg att ttc acc gaa gcc ctc cac agc 691  
 Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr Glu Ala Leu His Ser  
 185 190 195

gaa gcc gac ttc cga tac ttc cgg cac gcc atc cct gat gcc ttg ttg 739  
 Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile Pro Asp Ala Leu Leu  
 200 205 210

ctg gcg aat atg acc gaa ttt ggc aaa acg acg ctg ctg tca gcc gac 787  
 Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr Leu Leu Ser Ala Asp  
 215 220 225

gtg ttg gaa gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg 835  
 Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr  
 230 235 240 245

ctg cgt att gcc atg gga caa gta gaa caa gca cta gcc gaa atc aaa 883  
 Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys  
 250 255 260

gaa cac ggt acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc 931  
 Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser  
 265 270 275

aga tta tat gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag 979  
 Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln  
 280 285 290

cac att ttc acc tac aga aaa gga gaa aac aat gag tgacagccaa 1025  
 His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn Glu  
 295 300 305

gtccgcaaag gac 1038

<210> 622  
 <211> 305  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 622  
 Met Asn Leu Phe Ser Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala  
 1 5 10 15  
 Phe Lys Ala Ala Leu Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala  
 20 25 30  
 Phe Ser Pro Leu Ile Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly  
 35 40 45  
 Val Tyr Val Ser Gly Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp  
 50 55 60  
 Ile Gly Leu Thr Thr Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile  
 65 70 75 80



Ala Arg Val Thr Asp Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe  
85 90 95

Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala  
100 105 110

Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys  
115 120 125

Gly His Leu Asp Gly Lys Glu Val Val Arg Thr Asp Val Met Val Arg  
130 135 140

Arg Ile Ala Ala Ala Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile  
145 150 155 160

Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile  
165 170 175

Glu Arg Ala Lys Ala Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr  
180 185 190

Glu Ala Leu His Ser Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile  
195 200 205

Pro Asp Ala Leu Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr  
210 215 220

Leu Leu Ser Ala Asp Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile  
225 230 235 240

Tyr Pro Val Thr Thr Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala  
245 250 255

Leu Ala Glu Ile Lys Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg  
260 265 270

Met Gln His Arg Ser Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr  
275 280 285

Asn Val Phe Asp Gln His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn  
290 295 300

Glu  
305

<210> 623  
<211> 242  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (1)..(219)  
<223> FRXA02333

<400> 623  
gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg ctg cgt att 48  
Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr Leu Arg Ile  
1 5 10 15

gcc atg gga caa gta gaa caa gca cta gcc gaa atc aaa gaa cac ggt 96  
 Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys Glu His Gly  
                   20                                  25                                  30

acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc aga tta tat 144  
 Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser Arg Leu Tyr  
                   35                                  40                                  45

gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag cac att ttc 192  
 Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln His Ile Phe  
                   50                                  55                                  60

acc tac aga aaa gga gaa aac aat gag tgacagccaa gtccgcaaag 239  
 Thr Tyr Arg Lys Gly Glu Asn Asn Glu  
                   65                                  70

gac 242

<210> 624  
 <211> 73  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 624  
 Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr Leu Arg Ile  
   1                                  5                                  10                                  15

Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys Glu His Gly  
                   20                                  25                                  30

Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser Arg Leu Tyr  
                   35                                  40                                  45

Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln His Ile Phe  
                   50                                  55                                  60

Thr Tyr Arg Lys Gly Glu Asn Asn Glu  
                   65                                  70

<210> 625  
 <211> 513  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(490)  
 <223> RXA00030

<400> 625  
 taaaaacgcc actttggtgt cgataacacc gaacttccga acataaaaga tgcgttggtg 60

ctctctgcac aatgtttctt tcggaactat tctggcgacc atg cga att gaa atc 115  
   Met Arg Ile Glu Ile  
   1                                  5

aca agc gta ttt gtt gat gac cag gcc aaa gca ctc gat ttc tac acc 163  
 Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala Leu Asp Phe Tyr Thr  
                   10                                  15                                  20

acg aag ctc gga ttt gag ctc aaa cac gat gta act gct ggt gac tac 211  
 Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val Thr Ala Gly Asp Tyr  
 25 30 35  
 cgc tgg ttg act gtt gtt gat cca gaa aac cca gat ggt gtg cag ctt 259  
 Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro Asp Gly Val Gln Leu  
 40 45 50  
 ttg ttg gaa cca aac cag cac cca gat gca gcg act tac caa gct gga 307  
 Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala Thr Tyr Gln Ala Gly  
 55 60 65  
 att aaa cga gac ggt att ccc gct aca cag ttt tat gtt gat gat gtg 355  
 Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe Tyr Val Asp Asp Val  
 70 75 80 85  
 cag gaa gaa tat gac agc ctc aag gat aaa ggc gtg gat ttc atc atg 403  
 Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly Val Asp Phe Ile Met  
 90 95 100  
 gaa cca acc gat gtg ggc cct tca gtg att gcc att ctc gat gac acc 451  
 Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala Ile Leu Asp Asp Thr  
 105 110 115  
 gta gga aac cta att cag att gtt caa ttg aag cag aac taacccccgtg 500  
 Val Gly Asn Leu Ile Gln Ile Val Gln Leu Lys Gln Asn  
 120 125 130  
 gaatgacaaa atc 513

&lt;210&gt; 626

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 626

Met Arg Ile Glu Ile Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala  
 1 5 10 15  
 Leu Asp Phe Tyr Thr Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val  
 20 25 30  
 Thr Ala Gly Asp Tyr Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro  
 35 40 45  
 Asp Gly Val Gln Leu Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala  
 50 55 60  
 Thr Tyr Gln Ala Gly Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe  
 65 70 75 80  
 Tyr Val Asp Asp Val Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly  
 85 90 95  
 Val Asp Phe Ile Met Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala  
 100 105 110  
 Ile Leu Asp Asp Thr Val Gly Asn Leu Ile Gln Ile Val Gln Leu Lys  
 115 120 125

Gln Asn  
130

<210> 627  
<211> 2334  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(2311)  
<223> RXN00148

<400> 627  
ctttgagggc agcgcgcatg cgcccgatgg ttatttgaac atgacaattg atgccgcggc 60  
gacgctggct gacctgctag atgctttggg agcttaaatac atg acg tcg atc cct 115  
Met Thr Ser Ile Pro  
1 5  
aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163  
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser  
10 15 20  
cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211  
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp  
25 30 35  
gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg 259  
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala  
40 45 50  
gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg 307  
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly  
55 60 65  
ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355  
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr  
70 75 80 85  
gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac 403  
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn  
90 95 100  
ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc 451  
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr  
105 110 115  
cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt 499  
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly  
120 125 130  
atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt 547  
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe  
135 140 145  
gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc 595  
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly  
150 155 160 165

gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa	643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln	
170 175 180	
ggg gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg	691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu	
185 190 195	
aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg	739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser	
200 205 210	
atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aag atg cca	787
Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro	
215 220 225	
cgt ttt aac tcc att tcg att tct ggc tat cac atc cag gaa gcg gga	835
Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly	
230 235 240 245	
gcg act gcc gat ttg gag ctg gcc tac act ctg gcg gat ggt att gaa	883
Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu	
250 255 260	
tac atc cgt gca ggt aaa gag gta ggc ctt gac gtg gat aag ttc gcg	931
Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala	
265 270 275	
cct cgt ctg tcc ttc ttc tgg ggt att tct atg tac acc ttc atg gag	979
Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
280 285 290	
atc gca aag ctg cgt gcg gga cga ctg ctg tgg agc gag ttg gtg gca	1027
Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala	
295 300 305	
aaa ttc gat ccg aaa aac gcc aag tcc cag tcg ctg cgc acg cac tcg	1075
Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
310 315 320 325	
cag acc tct ggt tgg tcg ttg acc gcg cag gat gtg tac aac aac gtc	1123
Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val	
330 335 340	
gcc cgc acc gcg att gag gcg atg gct gca acc cag ggc cac acc cag	1171
Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln	
345 350 355	
tcg ctg cac acc aat gca ctt gat gag gcg ttg gcg ctg ccc acc gat	1219
Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp	
360 365 370	
ttc tct gct cgt atc gcc cga aac acc cag ctg ttg ctg cag cag gaa	1267
Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Leu Gln Gln Glu	
375 380 385	
tct ggc acg gtg cgt cca gtt gat cca tgg gcg ggc tcc tat tac gtg	1315
Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala Gly Ser Tyr Tyr Val	
390 395 400 405	

gag tgg ttg acc aat gag ctg gct aac cgc gcg cgc aag cac atc gat	1363
Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala Arg Lys His Ile Asp	
410 415 420	
gag gtg gag gaa gcc ggc gga atg gcg cag gcc acc gcg cag gga att	1411
Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala Thr Ala Gln Gly Ile	
425 430 435	
cct aag ctg cgc att gag gaa tca gcg gca cgc acc cag gct cgc att	1459
Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg Thr Gln Ala Arg Ile	
440 445 450	
gat tcc ggc cgc cag gcg ctg atc ggc gtg aat cgc tac gtg gcg gaa	1507
Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu	
455 460 465	
gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc	1555
Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg	
470 475 480 485	
gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat	1603
Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp	
490 495 500	
gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac	1651
Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Ala Arg Asn	
505 510 515	
gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc	1699
Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala	
520 525 530	
gtc gat gct gcg cgc gca aaa gct acc att gga gag atc tcc gat gct	1747
Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala	
535 540 545	
ttg gaa gtt gtc ttt ggc cgc cac gaa gca gaa atc agg acg ctg tct	1795
Leu Glu Val Val Phe Gly Arg His Glu Ala Glu Ile Arg Thr Leu Ser	
550 555 560 565	
ggc gtg tac aag gat gag gtt gga aag gaa ggc aca gtg agc aac gtc	1843
Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val	
570 575 580	
gaa cgc gcg atc gcc ctg gct gac gcc ttt gag gct gag gaa ggc cgc	1891
Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg	
585 590 595	
cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt	1939
Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg	
600 605 610	
gga cag aag gtt gtc gcg tct gcc tat gct gac ctg ggc atg gac gtg	1987
Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val	
615 620 625	
gat gtt gga ccg ctg ttt caa act cca gcc gaa gct gcc cgc gcc gcc	2035
Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala	
630 635 640 645	
gtg gac gcc gat gtt cac gtg gtg ggt atg tct tcg ctg gca gca ggc	2083

Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly  
650 655 660

cac ctc acc ttg ctg ccc gag ctg aag aaa gaa ctt gca gct ctt ggc 2131  
His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly  
665 670 675

cgc gat gac att ctg gtc acc gtg ggc ggc gtc att ccg ccg ggc gat 2179  
Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val Ile Pro Pro Gly Asp  
680 685 690

ttc cag gat ctc tac gat atg ggt gcc gcc gcg att tac cct tca gga 2227  
Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly  
695 700 705

acc gtc atc gcg gag tcg gcg atc gat ctg atc acc cga ctc gcc gca 2275  
Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile Thr Arg Leu Ala Ala  
710 715 720 725

cac ctg ggc ttt gac ctg gat gtg gat gtg aat gaa tgatcacggt 2321  
His Leu Gly Phe Asp Leu Asp Val Asp Val Asn Glu  
730 735

ttcctagaag aca 2334

&lt;210&gt; 628

&lt;211&gt; 737

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 628

Met Thr Ser Ile Pro Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr  
1 5 10 15

Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr  
20 25 30

Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp  
35 40 45

Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys  
50 55 60

Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp  
65 70 75 80

Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala  
85 90 95

Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala  
100 105 110

Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val  
115 120 125

Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp  
130 135 140

Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser  
145 150 155 160

Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val  
 165 170 175  
 Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile  
 180 185 190  
 Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr  
 195 200 205  
 Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr  
 210 215 220  
 Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His  
 225 230 235 240  
 Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu  
 245 250 255  
 Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp  
 260 265 270  
 Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met  
 275 280 285  
 Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp  
 290 295 300  
 Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser  
 305 310 315 320  
 Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp  
 325 330 335  
 Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr  
 340 345 350  
 Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu  
 355 360 365  
 Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu  
 370 375 380  
 Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala  
 385 390 395 400  
 Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala  
 405 410 415  
 Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala  
 420 425 430  
 Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg  
 435 440 445  
 Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn  
 450 455 460  
 Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp  
 465 470 475 480



Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys  
                   485                                  490                                  495  
 Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr  
                   500                                  505                                  510  
 Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn  
                   515                                  520                                  525  
 Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly  
                   530                                  535                                  540  
 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu  
 545                                  550                                  555                                  560  
 Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly  
                   565                                  570                                  575  
 Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu  
                   580                                  585                                  590  
 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln  
                   595                                  600                                  605  
 Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp  
                   610                                  615                                  620  
 Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu  
 625                                  630                                  635                                  640  
 Ala Ala Arg Ala Ala Val Asp Ala Asp Val His Val Val Gly Met Ser  
                   645                                  650                                  655  
 Ser Leu Ala Ala Gly His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu  
                   660                                  665                                  670  
 Leu Ala Ala Leu Gly Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val  
                   675                                  680                                  685  
 Ile Pro Pro Gly Asp Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala  
                   690                                  695                                  700  
 Ile Tyr Pro Ser Gly Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile  
 705                                  710                                  715                                  720  
 Thr Arg Leu Ala Ala His Leu Gly Phe Asp Leu Asp Val Asp Val Asn  
                   725                                  730                                  735

Glu

<210> 629  
 <211> 2098  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2098)  
 <223> FRXA00148

<400>	629	
ctttgagggc agcgcgcatg cgcccgatgg ttatttgaac atgacaattg atgccgcggc	60	
gacgctgggt gacctgctag atgctttggg agcttaaatac		115
	Met Thr Ser Ile Pro	
	1 5	
aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca		163
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser		
	10 15 20	
cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat		211
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp		
	25 30 35	
gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg		259
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala		
	40 45 50	
gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg		307
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly		
	55 60 65	
ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac		355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr		
	70 75 80 85	
gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac		403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn		
	90 95 100	
ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc		451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr		
	105 110 115	
cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt		499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly		
	120 125 130	
atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt		547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe		
	135 140 145	
gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc		595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly		
	150 155 160 165	
gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa		643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln		
	170 175 180	
ggt gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg		691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu		
	185 190 195	
aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg		739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser		
	200 205 210	
atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aaq atg cca		787

Met	Arg	Ile	Ile	Ser	Asn	Ile	Phe	Glu	Tyr	Thr	Ser	Leu	Lys	Met	Pro		
215						220					225						
cgt	ttt	aac	tcc	att	tcg	att	tct	ggc	tat	cac	atc	cag	gaa	gcg	gga	835	
Arg	Phe	Asn	Ser	Ile	Ser	Ile	Ser	Gly	Tyr	His	Ile	Gln	Glu	Ala	Gly		
230					235				240						245		
gcg	act	gcc	gat	ttg	gag	ctg	gcc	tac	act	ctg	gcg	gat	ggt	att	gaa	883	
Ala	Thr	Ala	Asp	Leu	Glu	Leu	Ala	Tyr	Thr	Leu	Ala	Asp	Gly	Ile	Glu		
				250					255					260			
tac	atc	cgt	gca	ggt	aaa	gag	gta	ggc	ctt	gac	gtg	gat	aag	ttc	gcg	931	
Tyr	Ile	Arg	Ala	Gly	Lys	Glu	Val	Gly	Leu	Asp	Val	Asp	Lys	Phe	Ala		
			265					270					275				
cct	cgt	ctg	tcc	ttc	ttc	tgg	ggt	att	tct	atg	tac	acc	ttc	atg	gag	979	
Pro	Arg	Leu	Ser	Phe	Phe	Trp	Gly	Ile	Ser	Met	Tyr	Thr	Phe	Met	Glu		
		280					285					290					
atc	gca	aag	ctg	cgt	gcg	gga	cga	ctg	ctg	tgg	agc	gag	ttg	gtg	gca	1027	
Ile	Ala	Lys	Leu	Arg	Ala	Gly	Arg	Leu	Leu	Trp	Ser	Glu	Leu	Val	Ala		
	295					300					305						
aaa	ttc	gat	ccg	aaa	aac	gcc	aag	tcc	cag	tcg	ctg	cgc	acg	cac	tcg	1075	
Lys	Phe	Asp	Pro	Lys	Asn	Ala	Lys	Ser	Gln	Ser	Leu	Arg	Thr	His	Ser		
310					315				320						325		
cag	acc	tct	ggt	tgg	tcg	ttg	acc	gcg	cag	gat	gtg	tac	aac	aac	gtc	1123	
Gln	Thr	Ser	Gly	Trp	Ser	Leu	Thr	Ala	Gln	Asp	Val	Tyr	Asn	Asn	Val		
				330					335					340			
gcc	cgc	acc	gcg	att	gag	gcg	atg	gct	gca	acc	cag	ggc	cac	acc	cag	1171	
Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr	Gln	Gly	His	Thr	Gln		
			345					350					355				
tcg	ctg	cac	acc	aat	gca	ctt	gat	gag	gcg	ttg	gcg	ctg	ccc	acc	gat	1219	
Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Leu	Pro	Thr	Asp		
		360					365					370					
ttc	tct	gct	cgt	atc	gcc	cga	aac	acc	cag	ctg	ttg	ctg	cag	cag	gaa	1267	
Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu	Leu	Leu	Gln	Gln	Glu		
	375					380					385						
tct	ggc	acg	gtg	cgt	cca	gtt	gat	cca	tgg	gcg	ggc	tcc	tat	tac	gtg	1315	
Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala	Gly	Ser	Tyr	Tyr	Val		
390					395				400						405		
gag	tgg	ttg	acc	aat	gag	ctg	gct	aac	cgc	gcg	cgc	aag	cac	atc	gat	1363	
Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala	Arg	Lys	His	Ile	Asp		
				410				415						420			
gag	gtg	gag	gaa	gcc	ggc	gga	atg	gcg	cag	gcc	acc	gcg	cag	gga	att	1411	
Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala	Thr	Ala	Gln	Gly	Ile		
			425					430					435				
cct	aag	ctg	cgc	att	gag	gaa	tca	gcg	gca	cgc	acc	cag	gct	cgc	att	1459	
Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg	Thr	Gln	Ala	Arg	Ile		
		440					445					450					
gat	tcc	ggc	cgc	cag	gcg	ctg	atc	ggc	gtg	aat	cgc	tac	gtg	gcg	gaa	1507	
Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn	Arg	Tyr	Val	Ala	Glu		

455	460	465	
gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg 470 475 480 485			1555
gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp 490 495 500			1603
gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Ala Arg Asn 505 510 515			1651
gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala 520 525 530			1699
gtc gat gct gcg cgc gca aaa gct acc att gga gag atc tcc gat gct Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala 535 540 545			1747
ttg gaa gtt gtc ttt ggc cgc cac gaa gca gaa atc agg acg ctg tct Leu Glu Val Val Phe Gly Arg His Glu Ala Glu Ile Arg Thr Leu Ser 550 555 560 565			1795
ggc gtg tac aag gat gag gtt gga aag gaa ggc aca gtg agc aac gtc Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val 570 575 580			1843
gaa cgc gcg atc gcc ctg gct gac gcc ttt gag gct gag gaa ggc cgc Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg 585 590 595			1891
cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg 600 605 610			1939
gga cag aag gtt gtc gcg tct gcc tat gct gac ctg ggc atg gac gtg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val 615 620 625			1987
gat gtt gga ccg ctg ttt caa act cca gcc gaa gct gcc cgc gcc gcc Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala 630 635 640 645			2035
gtg gac gcc gat gtt cac gtg gtg ggt atg tct tcg ctg gca gca ggc Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly 650 655 660			2083
cac ctc acc ttg ctg His Leu Thr Leu Leu 665			2098

&lt;210&gt; 630

&lt;211&gt; 666

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 630

Met Thr Ser Ile Pro Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr  
 1 5 10 15  
 Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr  
 20 25 30  
 Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp  
 35 40 45  
 Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys  
 50 55 60  
 Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp  
 65 70 75 80  
 Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala  
 85 90 95  
 Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala  
 100 105 110  
 Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val  
 115 120 125  
 Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp  
 130 135 140  
 Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser  
 145 150 155 160  
 Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val  
 165 170 175  
 Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile  
 180 185 190  
 Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr  
 195 200 205  
 Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr  
 210 215 220  
 Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His  
 225 230 235 240  
 Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu  
 245 250 255  
 Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp  
 260 265 270  
 Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met  
 275 280 285  
 Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp  
 290 295 300  
 Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser  
 305 310 315 320  
 Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp

325										330					335				
Val	Tyr	Asn	Asn	Val	Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr				
			340					345					350						
Gln	Gly	His	Thr	Gln	Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu				
		355					360					365							
Ala	Leu	Pro	Thr	Asp	Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu				
		370				375					380								
Leu	Leu	Gln	Gln	Glu	Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala				
					390					395					400				
Gly	Ser	Tyr	Tyr	Val	Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala				
				405					410					415					
Arg	Lys	His	Ile	Asp	Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala				
			420					425					430						
Thr	Ala	Gln	Gly	Ile	Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg				
			435				440					445							
Thr	Gln	Ala	Arg	Ile	Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn				
						455					460								
Arg	Tyr	Val	Ala	Glu	Glu	Asp	Glu	Glu	Ile	Glu	Val	Leu	Lys	Val	Asp				
					470					475					480				
Asn	Thr	Lys	Val	Arg	Ala	Glu	Gln	Leu	Ala	Lys	Leu	Ala	Gln	Leu	Lys				
				485				490						495					
Ala	Glu	Arg	Asn	Asp	Ala	Glu	Val	Lys	Ala	Ala	Leu	Asp	Ala	Leu	Thr				
				500				505					510						
Ala	Ala	Ala	Arg	Asn	Glu	His	Lys	Glu	Pro	Gly	Asp	Leu	Asp	Gln	Asn				
							520					525							
Leu	Leu	Lys	Leu	Ala	Val	Asp	Ala	Ala	Arg	Ala	Lys	Ala	Thr	Ile	Gly				
						535					540								
Glu	Ile	Ser	Asp	Ala	Leu	Glu	Val	Val	Phe	Gly	Arg	His	Glu	Ala	Glu				
					550					555					560				
Ile	Arg	Thr	Leu	Ser	Gly	Val	Tyr	Lys	Asp	Glu	Val	Gly	Lys	Glu	Gly				
				565					570					575					
Thr	Val	Ser	Asn	Val	Glu	Arg	Ala	Ile	Ala	Leu	Ala	Asp	Ala	Phe	Glu				
				580				585					590						
Ala	Glu	Glu	Gly	Arg	Arg	Pro	Arg	Ile	Phe	Ile	Ala	Lys	Met	Gly	Gln				
				595			600					605							
Asp	Gly	His	Asp	Arg	Gly	Gln	Lys	Val	Val	Ala	Ser	Ala	Tyr	Ala	Asp				
						615					620								
Leu	Gly	Met	Asp	Val	Asp	Val	Gly	Pro	Leu	Phe	Gln	Thr	Pro	Ala	Glu				
					630					635					640				
Ala	Ala	Arg	Ala	Ala	Val	Asp	Ala	Asp	Val	His	Val	Val	Gly	Met	Ser				
				645					650					655					

Ser Leu Ala Ala Gly His Leu Thr Leu Leu  
660 665

<210> 631  
<211> 1971  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1948)  
<223> RXA00149

<400> 631  
ttttcgtagg taaacacagg tgaaggcttt acaagcttgt gaactcccta cacaaaagca 60  
atccaatagc tatccataag caagagaaag taagtctacg ttg act gat ctc aca 115  
Leu Thr Asp Leu Thr  
1 5  
aag act gcg gtg ccc gag gaa ctt tca gag aac ctc gaa act tgg tac 163  
Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn Leu Glu Thr Trp Tyr  
10 15 20  
aag gct gtg gcc ggt gtt ttc gcg cgc aca cag aaa aaa gac atc ggc 211  
Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln Lys Lys Asp Ile Gly  
25 30 35  
gac att gcc gta gat gtg tgg aag aaa ctc atc gtc act aca ccg gat 259  
Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile Val Thr Thr Pro Asp  
40 45 50  
ggt gtt gat atc aat ccg ctg tac acc aga gca gat gag tcc cag agg 307  
Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala Asp Glu Ser Gln Arg  
55 60 65  
aaa ttc act gag gtt cct ggt gag ttt ccc ttc act agg gga acc act 355  
Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe Thr Arg Gly Thr Thr  
70 75 80 85  
gtt gat ggt gaa cgc gtt ggt tgg ggt gtt act gag act ttc gga cat 403  
Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr Glu Thr Phe Gly His  
90 95 100  
gac agc ccg aag aat atc aac gct gcg gtg ctg aat gct ctg aat tct 451  
Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu Asn Ala Leu Asn Ser  
105 110 115  
ggc acc acc aca ttg ggt ttt gag ttc tct gag gaa ttc acg gca gct 499  
Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu Glu Phe Thr Ala Ala  
120 125 130  
gat ctt aaa gtt gct ctc gaa ggc gtg tat ctc aac atg gct ccg ttg 547  
Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu Asn Met Ala Pro Leu  
135 140 145  
ctg att cat gcg ggt gga tcc acg tca gag gtt gca gcg gcg ttg tat 595  
Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val Ala Ala Ala Leu Tyr  
150 155 160 165

acg ttg gcg gag gaa gcc gga acg ttt ttt gct gcg ttg acc ttg ggt	643
Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala Ala Leu Thr Leu Gly	
170 175 180	
tct cgt cct ttg acg gcg cag gtt gat ggt tcg cac agt gac acc att	691
Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser His Ser Asp Thr Ile	
185 190 195	
gaa gaa gca gtt cag ttg gca gtg aat gct tcc aag cgt gcg aat gtg	739
Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser Lys Arg Ala Asn Val	
200 205 210	
cgc gct atc ttg gtg gat ggt tcc agt ttt tcc aac cag ggc gcg tcg	787
Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser Asn Gln Gly Ala Ser	
215 220 225	
gat gct caa gaa att ggt cta agt atc gcc gcc ggt gtg gat tat gtc	835
Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala Gly Val Asp Tyr Val	
230 235 240 245	
cgt cgc ttg gtc gat gca ggc ctt tcc acg gaa gct gca ctt aag cag	883
Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu Ala Ala Leu Lys Gln	
250 255 260	
gtg gcg ttc cgt ttt gcg gtc acc gat gag cag ttc gcg cag att tct	931
Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln Phe Ala Gln Ile Ser	
265 270 275	
aag ctg cgt gtg gct cga cgt ctg tgg gcc agg gtg tgt gag gtg ctt	979
Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg Val Cys Glu Val Leu	
280 285 290	
ggt ttt cca gag ctg gcc gta gca cca cag cat gcg gtg act gca cga	1027
Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His Ala Val Thr Ala Arg	
295 300 305	
gcg atg ttt agc cag cgt gat ccg tgg gtg aat atg ctg cgc agt act	1075
Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn Met Leu Arg Ser Thr	
310 315 320 325	
gtt gca gct ttc gct gca ggc gtc ggt gga gca acc gat gtg gag gtt	1123
Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala Thr Asp Val Glu Val	
330 335 340	
cgt act ttt gat gat gcg atc cca gat gga gtt cct gga gtg tcg agg	1171
Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val Pro Gly Val Ser Arg	
345 350 355	
aat ttc gct cac cgc atc gcg cgc aat act aat ttg ttg ttg cta gaa	1219
Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn Leu Leu Leu Leu Glu	
360 365 370	
gag tca cat ctt ggt cac gtg gtt gat cct gct ggt gga tca tat ttc	1267
Glu Ser His Leu Gly His Val Asp Pro Ala Gly Gly Ser Tyr Phe	
375 380 385	
gtg gag agc ttc acc gat gat cta gcg gag aag gcg tgg gct gtg ttc	1315
Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys Ala Trp Ala Val Phe	
390 395 400 405	



```

agt ggc atc gaa gct gag ggc gga tac agt gca gct tgt gca tcc ggc 1363
Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala Ala Cys Ala Ser Gly
                               410                               415                               420

acg gtg act gcc atg ctt gat cag acg tgg gag cag act cgc gct gat 1411
Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu Gln Thr Arg Ala Asp
                               425                               430                               435

gtg gcg tcg aga aag aag aag ctc act gga att aat gag ttc ccg aac 1459
Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile Asn Glu Phe Pro Asn
                               440                               445                               450

ttg gcg gag tct ccg ctg cca gct gat cgt cgg gta gaa cct gca ggt 1507
Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg Val Glu Pro Ala Gly
                               455                               460                               465

gtg cgt cga tgg gca gcg gat ttt gaa gcg ctg cgc aat cgt tcg gat 1555
Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu Arg Asn Arg Ser Asp
                               470                               475                               480                               485

gct ttc ttg gaa aag aac ggc gcg agg cca cag atc acg atg att cct 1603
Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln Ile Thr Met Ile Pro
                               490                               495                               500

ctg gga ccg ttg tcc aag cac aat att cgc act ggt ttt act tcc aac 1651
Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr Gly Phe Thr Ser Asn
                               505                               510                               515

ctg ttg gct tcc ggt ggc att gaa gca atc aac ccg ggt caa ctt gtt 1699
Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn Pro Gly Gln Leu Val
                               520                               525                               530

ccc ggc act gac gct ttt gca gaa gct gca cag gcc gca ggc att gta 1747
Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln Ala Ala Gly Ile Val
                               535                               540                               545

gtg gtg tgt gga acg gac caa gag tat gcc gaa acg ggg gag gga gcc 1795
Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu Thr Gly Glu Gly Ala
                               550                               555                               560                               565

gtc gaa aag ctc cgc gaa gcg ggc gtt gag cgc atc ctg ctt gct ggc 1843
Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg Ile Leu Leu Ala Gly
                               570                               575                               580

gcg ccg aag agc ttt gag ggc agc gcg cat gcg ccc gat ggt tat ttg 1891
Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala Pro Asp Gly Tyr Leu
                               585                               590                               595

aac atg aca att gat gcc gcg gcg acg ctg gct gac ctg cta gat gct 1939
Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala Asp Leu Leu Asp Ala
                               600                               605                               610

ttg gga gct taaatcatga cgtcgatccc taa 1971
Leu Gly Ala
                               615

```

&lt;210&gt; 632

&lt;211&gt; 616

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

<400> 632  
 Leu Thr Asp Leu Thr Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn  
 1 5 10 15  
 Leu Glu Thr Trp Tyr Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln  
 20 25 30  
 Lys Lys Asp Ile Gly Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile  
 35 40 45  
 Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala  
 50 55 60  
 Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe  
 65 70 75 80  
 Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr  
 85 90 95  
 Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu  
 100 105 110  
 Asn Ala Leu Asn Ser Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu  
 115 120 125  
 Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu  
 130 135 140  
 Asn Met Ala Pro Leu Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val  
 145 150 155 160  
 Ala Ala Ala Leu Tyr Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala  
 165 170 175  
 Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser  
 180 185 190  
 His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser  
 195 200 205  
 Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser  
 210 215 220  
 Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala  
 225 230 235 240  
 Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu  
 245 250 255  
 Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln  
 260 265 270  
 Phe Ala Gln Ile Ser Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg  
 275 280 285  
 Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His  
 290 295 300  
 Ala Val Thr Ala Arg Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn  
 305 310 315 320

Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala  
 325 330 335  
 Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val  
 340 345 350  
 Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn  
 355 360 365  
 Leu Leu Leu Leu Glu Glu Ser His Leu Gly His Val Val Asp Pro Ala  
 370 375 380  
 Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys  
 385 390 395 400  
 Ala Trp Ala Val Phe Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala  
 405 410 415  
 Ala Cys Ala Ser Gly Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu  
 420 425 430  
 Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile  
 435 440 445  
 Asn Glu Phe Pro Asn Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg  
 450 455 460  
 Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu  
 465 470 475 480  
 Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln  
 485 490 495  
 Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr  
 500 505 510  
 Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn  
 515 520 525  
 Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln  
 530 535 540  
 Ala Ala Gly Ile Val Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu  
 545 550 555 560  
 Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg  
 565 570 575  
 Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala  
 580 585 590  
 Pro Asp Gly Tyr Leu Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala  
 595 600 605  
 Asp Leu Leu Asp Ala Leu Gly Ala  
 610 615

&lt;210&gt; 633

&lt;211&gt; 777

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(754)

&lt;223&gt; RXN00317

&lt;400&gt; 633

```

caacggttac atcactcacg cattaactcc cctgggtggt accgcatggt cgtttcccaa 60

gtctagccaa gccttgaaaa attctggcaa ggttaatggt gtg act acg cct tct 115
                               Val Thr Thr Pro Ser
                               1 5

aag aaa act ctg ctc ttt gat ctc gac gga acc ctc gtc gat tct ttc 163
Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
                               10 15 20

ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg 211
Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp
                               25 30 35

gaa atc ccc tct gag gaa cgc atc tcg caa gtt cca gga cct ccc atg 259
Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met
                               40 45 50

gaa tgg acg ttc cag gat ttg ggc atg act cca gag cag gca caa gac 307
Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp
                               55 60 65

gct ctg cag acc tac ctt gag cat tac ggc cag gtg ggt tgg gat ctt 355
Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu
                               70 75 80 85

tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc cgc ttg aaa tac 403
Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Arg Leu Lys Tyr
                               90 95 100

gaa ggt ttc cgt ctg tgc acc gcc acc tcc aag ggc gag ttc ttt gcg 451
Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys Gly Glu Phe Phe Ala
                               105 110 115

gag aag gta ctt cgc aaa ttc gag atg ttc gat ctc ttc gaa ttc atg 499
Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp Leu Phe Glu Phe Met
                               120 125 130

ggt gcc gcc acc gac agc ggc aac cga cgc agc aaa tct gcc gtg atc 547
Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser Lys Ser Ala Val Ile
                               135 140 145

aaa cat gtc ctc gac agc gtt ggg ttg gac gaa cca aat gat att ttg 595
Lys His Val Leu Asp Ser Val Gly Leu Asp Glu Pro Asn Asp Ile Leu
                               150 155 160 165

atg att ggt gat cga tca cac gat att gaa ggt tcg agt gaa ttc ggc 643
Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly Ser Ser Glu Phe Gly
                               170 175 180

atc gat tgt gtt gcc gta acc tgg ggc tac ggc agc aaa act gaa tgg 691
Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly Ser Lys Thr Glu Trp

```

185 190 195  
gac gct gcc cgc tac acc gtg agc acc gca gaa gaa tta gaa agg atc 739  
Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu Glu Leu Glu Arg Ile  
200 205 210

atc cat gac tgg gcc taaaacttcg ctacctgtgg aaa 777  
Ile His Asp Trp Ala  
215

<210> 634

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 634

Val Thr Thr Pro Ser Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr  
1 5 10 15

Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu  
20 25 30

His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val  
35 40 45

Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro  
50 55 60

Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln  
65 70 75 80

Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu  
85 90 95

Ile Arg Leu Lys Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys  
100 105 110

Gly Glu Phe Phe Ala Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp  
115 120 125

Leu Phe Glu Phe Met Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser  
130 135 140

Lys Ser Ala Val Ile Lys His Val Leu Asp Ser Val Gly Leu Asp Glu  
145 150 155 160

Pro Asn Asp Ile Leu Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly  
165 170 175

Ser Ser Glu Phe Gly Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly  
180 185 190

Ser Lys Thr Glu Trp Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu  
195 200 205

Glu Leu Glu Arg Ile Ile His Asp Trp Ala  
210 215

<210> 635

<211> 439  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(439)  
 <223> FRXA00317

<400> 635  
 caacgggttac atcactcacg cattacctcc cctgggttggt accgcatggt cgtttcccaa 60  
 gtcaagccaa gccttgaaaa attctggcaa ggttaatggt gtg act acg cct tct 115  
 Val Thr Thr Pro Ser  
 1 5  
 aag aaa act ctg ctc ttt gat ctc gac gga acc ctc gtc gat tct ttc 163  
 Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe  
 10 15 20  
 ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg 211  
 Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp  
 25 30 35  
 gaa atc ccc tct gag gaa cgc atc tcg caa gtt cca gga cct ccc atg 259  
 Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met  
 40 45 50  
 gaa tgg acg ttc cag gat ttg ggc atg act cca gag cag gca caa gac 307  
 Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp  
 55 60 65  
 gct ctg cag acc tac ctt gag cat tac ggc cag gtg ggt tgg gat ctt 355  
 Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu  
 70 75 80 85  
 tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc ccc ttg ata tac 403  
 Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Pro Leu Ile Tyr  
 90 95 100  
 gaa ggt ttt cgt ctg tgc acc gcc acc ttt caa ggg 439  
 Glu Gly Phe Arg Leu Cys Thr Ala Thr Phe Gln Gly  
 105 110

<210> 636  
 <211> 113  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 636  
 Val Thr Thr Pro Ser Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr  
 1 5 10 15  
 Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu  
 20 25 30  
 His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val  
 35 40 45  
 Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro

Gly

```
<220>  
<221> CDS  
<222> (101)..(793)  
<223> RXA02196
```

913

Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu Phe Phe Ile Gly Ser  
 120 125 130

atc gct ggt gat gaa gtc cca aca gca aag cca gcc ccc gac atg tac 547  
 Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro Ala Pro Asp Met Tyr  
 135 140 145

ctc gaa gca gca cga cgt gtg ggc ttt gac cca tca gag tgc ctc gtg 595  
 Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro Ser Glu Cys Leu Val  
 150 155 160 165

ttc gaa gat tcc tac aac ggc atg ctg ggc gct gtt act gca ggt tgc 643  
 Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala Val Thr Ala Gly Cys  
 170 175 180

cgc gtc att ggt ctg cac cca gaa gaa gtc caa gcg cca gaa ggt gta 691  
 Arg Val Ile Gly Leu His Pro Glu Glu Val Gln Ala Pro Glu Gly Val  
 185 190 195

gtg cct ttg cgt tcc ctc cac ggt aaa aac tct ttc gaa ggt gtc acc 739  
 Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser Phe Glu Gly Val Thr  
 200 205 210

gct gag atg gtc act gcc tgg tac cac cag atc gag ccg gca ggt gtc 787  
 Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile Glu Pro Ala Gly Val  
 215 220 225

gca aaa taaaaccagg tgggggagtg aaa 816  
 Ala Lys  
 230

<210> 638  
 <211> 231  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 638  
 Met Ile Lys Ala Ile Phe Trp Asp Met Asp Gly Thr Met Val Asp Ser  
 1 5 10 15

Glu Pro Gln Trp Gly Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly  
 20 25 30

Arg Arg Leu Thr Pro Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu  
 35 40 45

Pro Arg Thr Met Arg Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser  
 50 55 60

Asp Ala Asp Tyr Glu Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His  
 65 70 75 80

Glu Leu Phe Asp Glu Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu  
 85 90 95

Leu Thr Glu Leu Lys Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn  
 100 105 110

Thr Glu Arg Asp Leu Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu  
 115 120 125



Phe Phe Ile Gly Ser Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro  
 130 135 140  
 Ala Pro Asp Met Tyr Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro  
 145 150 155 160  
 Ser Glu Cys Leu Val Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala  
 165 170 175  
 Val Thr Ala Gly Cys Arg Val Ile Gly Leu His Pro Glu Glu Val Gln  
 180 185 190  
 Ala Pro Glu Gly Val Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser  
 195 200 205  
 Phe Glu Gly Val Thr Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile  
 210 215 220  
 Glu Pro Ala Gly Val Ala Lys  
 225 230

<210> 639  
 <211> 531  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(508)  
 <223> RXN02461

<400> 639  
 agaaaatctc aaggcaaaaa acaagccacc ccaatctgtg cgacaatcaa accacagact 60  
 acgactatta tgtcacgaag aaaccaaaga aagggaata atg cgc gga cta att 115  
 Met Arg Gly Leu Ile  
 1 5  
 gtt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc 163  
 Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg  
 10 15 20  
 tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg 211  
 Trp Arg Asn Leu Leu Ala Ala Lys Lys Asn Gly Val Gly Thr Val  
 25 30 35  
 atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa 259  
 Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu  
 40 45 50  
 ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt 307  
 Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu  
 55 60 65  
 ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc 355  
 Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala  
 70 75 80 85  
 atc gac ctg ccc atg cgt gac tgc gtg ctt gtc gac gac tcg atc ctc 403

Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu  
                             90                            95                            100

aac gtg cgc ggc gcc gtc gaa gcc gga ctc gta ggc gtc tac tac cag 451  
 Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln  
                             105                            110                            115

caa ttt gac cgt gca gtc gtc gaa atc gtc gga ctg ttc ggg cta gaa 499  
 Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly Leu Phe Gly Leu Glu  
                             120                            125                            130

gga gaa ttc taatcttgcg cgtctacatc cca 531  
 Gly Glu Phe  
                             135

&lt;210&gt; 640

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 640

Met Arg Gly Leu Ile Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp  
   1                            5                            10                            15

Glu Asp Gln Arg Arg Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn  
                             20                            25                            30

Gly Val Gly Thr Val Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala  
                             35                            40                            45

Ala Pro Ile Arg Glu Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu  
   50                            55                            60

Leu Ser Gly Glu Leu Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln  
   65                            70                            75                            80

Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val  
                             85                            90                            95

Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val  
                             100                            105                            110

Gly Val Tyr Tyr Gln Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly  
                             115                            120                            125

Leu Phe Gly Leu Glu Gly Glu Phe  
   130                            135

&lt;210&gt; 641

&lt;211&gt; 1662

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1639)

&lt;223&gt; RXN01744

&lt;400&gt; 641

tcttattggt tcttcgtttt gtatcgataa atacaatcgg tttcctggct taataaggct 60

gttctgtca acctgcaatg gaagaggaag tgtacctagc gtg gat gtc gtc gac 115  
Val Asp Val Val Asp  
1 5

atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163  
Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe  
10 15 20

gtc cca ctg acc att ggc tta gcg ccg ctg gtc gca atc atg caa acg 211  
Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr  
25 30 35

ttt tgg caa gtt acc ggc aaa gag cac tgg tat cgg gcc aca aga ttt 259  
Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr Arg Ala Thr Arg Phe  
40 45 50

ttt ggc act gtg ctg ctc atc aac ttc gcg gtt ggt gta gca acg ggc 307  
Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val Gly Val Ala Thr Gly  
55 60 65

att gtg cag gag ttc cag ttc ggt atg aac tgg tcg gaa tat tcg cgt 355  
Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp Ser Glu Tyr Ser Arg  
70 75 80 85

ttc gtc ggt gat gtt ttc ggc gga ccg ctg gct ttg gag ggt ctt atc 403  
Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala Leu Glu Gly Leu Ile  
90 95 100

gcg ttc ttc ctt gag tct gta ttc ctg gga ctg tgg att ttc gga tgg 451  
Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu Trp Ile Phe Gly Trp  
105 110 115

ggg aag att cct ggt tgg ttg cac act gca tcc att tgg atc gtt gct 499  
Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser Ile Trp Ile Val Ala  
120 125 130

att gcg acg aat att tct gcc tat ttc atc atc gtg gcc aac tcg ttt 547  
Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile Val Ala Asn Ser Phe  
135 140 145

atg cag cat ccg gtg ggt gct gag tat aac cct gag act ggt cgt gcg 595  
Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro Glu Thr Gly Arg Ala  
150 155 160 165

gag ctt act gat ttt tgg gct ctt ctc aca aac tcc acc gcg ctg gct 643  
Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn Ser Thr Ala Leu Ala  
170 175 180

gcg ttc ccg cat gct gtt gcc ggt ggt ttt tta aca gct gga act ttc 691  
Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu Thr Ala Gly Thr Phe  
185 190 195

gtt ctc gga att tcg ggt tgg tgg att att cgt gcg cac cgt cag gcc 739  
Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg Ala His Arg Gln Ala  
200 205 210

aag aag gct gag tcg gaa atc gag tcg aag cat tcg atg cac agg ccc 787  
Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His Ser Met His Arg Pro  
215 220 225

gcg ttg tgg gtt ggt tgg tgg acc aca gtt gtc tct tcc gtg gcg ctg	835
Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val Ser Ser Val Ala Leu	
230 235 240 245	
ttc atc act ggc gat atc cag gcg aag ctc atg ttc gtg caa cag cca	883
Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met Phe Val Gln Gln Pro	
250 255 260	
atg aag atg gcg tgc gcg gaa tcc ttg tgt gaa acc gcc aca gat cca	931
Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu Thr Ala Thr Asp Pro	
265 270 275	
aac ttc tcc att ctg aca att ggt acg cac aac aac tgc gat acg gta	979
Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn Asn Cys Asp Thr Val	
280 285 290	
acc cac ctg atc gat gtt ccg ttt gtg ctt cca ttc ttg gct gaa gga	1027
Thr His Leu Ile Asp Val Pro Phe Val Leu Pro Phe Leu Ala Glu Gly	
295 300 305	
aaa ttc acc ggt gtg act ttg cag ggt gta aac cag ctc caa gct gca	1075
Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn Gln Leu Gln Ala Ala	
310 315 320 325	
gcg gag caa gca tac ggt cct ggc aac tac tcc cct aac ttg ttt gtc	1123
Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser Pro Asn Leu Phe Val	
330 335 340	
acc tac tgg tca ttc cgc gca atg atc ggc ctg atg ctt ggt tct ttg	1171
Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu Met Leu Gly Ser Leu	
345 350 355	
gct atc gct gcg att gcg tgg ctg ttg ctg cgt aag aag cgc aca cca	1219
Ala Ile Ala Ala Ile Ala Trp Leu Leu Arg Lys Lys Arg Thr Pro	
360 365 370	
act gga aag att gct cgt ctg ttc cag atc ggc agc ctc att gct atc	1267
Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly Ser Leu Ile Ala Ile	
375 380 385	
ccg ttc cca ttc ttg gcc aac tct gct ggt tgg atc ttc acc gag atg	1315
Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp Ile Phe Thr Glu Met	
390 395 400 405	
ggc cgc cag cct tgg gtg gtg cac ccg aac cct gaa tct gcc ggc gat	1363
Gly Arg Gln Pro Trp Val Val His Pro Asn Pro Glu Ser Ala Gly Asp	
410 415 420	
gcc cga aca gag atg atc cgg atg act gtt gat atg ggt gta tct gat	1411
Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp Met Gly Val Ser Asp	
425 430 435	
cat gcg cca tgg caa gtc tgg ctg act ctc att ggc ttc acg att ctc	1459
His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile Gly Phe Thr Ile Leu	
440 445 450	
tat ctc att ttg ttc gtg gtg tgg gtg tgg ctg att cgc cgc gca gtt	1507
Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu Ile Arg Arg Ala Val	
455 460 465	

ctg atc gga cca cca gag gaa ggc gct cca tcc gtg gag gca aag act 1555  
 Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser Val Glu Ala Lys Thr  
 470 475 480 485

gga ccg gca acc ccg att ggt tca gat atg ccc atg aca ccg ctg caa 1603  
 Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro Met Thr Pro Leu Gln  
 490 495 500

ttt act gcc gct gcc cca acc aca ggt gaa aag gaa taaccatgga 1649  
 Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys Glu  
 505 510

tctcaatacc ttt 1662

<210> 642

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 642

Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val  
 1 5 10 15

Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val  
 20 25 30

Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr  
 35 40 45

Arg Ala Thr Arg Phe Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val  
 50 55 60

Gly Val Ala Thr Gly Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp  
 65 70 75 80

Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala  
 85 90 95

Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu  
 100 105 110

Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser  
 115 120 125

Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile  
 130 135 140

Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro  
 145 150 155 160

Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn  
 165 170 175

Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu  
 180 185 190

Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg  
 195 200 205

Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His

210	215	220
Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val 225 230 235 240		
Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met 245 250 255		
Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu 260 265 270		
Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn 275 280 285		
Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu Pro 290 295 300		
Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn 305 310 315 320		
Gln Leu Gln Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser 325 330 335		
Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu 340 345 350		
Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg 355 360 365		
Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly 370 375 380		
Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp 385 390 395 400		
Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn Pro 405 410 415		
Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp 420 425 430		
Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile 435 440 445		
Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu 450 455 460		
Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser 465 470 475 480		
Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro 485 490 495		
Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys 500 505 510		
Glu		

&lt;210&gt; 643



Ala	Leu	Glu	Gly	Leu	Ile	Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly	
			20					25						30		
ctg	tgg	att	ttc	gga	tgg	ggg	aag	att	cct	ggt	tgg	ttg	cac	act	gca	144
Leu	Trp	Ile	Phe	Gly	Trp	Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala	
			35				40					45				
tcc	att	tgg	atc	gtt	gct	att	gcg	acg	aat	att	tct	gcc	tat	ttc	atc	192
Ser	Ile	Trp	Ile	Val	Ala	Ile	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile	
		50				55					60					
atc	gtg	gcc	aac	tcg	ttt	atg	cag	cat	ccg	gtg	ggt	gct	gag	tat	aac	240
Ile	Val	Ala	Asn	Ser	Phe	Met	Gln	His	Pro	Val	Gly	Ala	Glu	Tyr	Asn	
	65				70				75						80	
cct	gag	act	ggt	cgt	gcg	gag	ctt	act	gat	ttt	tgg	gct	ctt	ctc	aca	288
Pro	Glu	Thr	Gly	Arg	Ala	Glu	Leu	Thr	Asp	Phe	Trp	Ala	Leu	Leu	Thr	
				85					90					95		
aac	tcc	acc	gcg	ctg	gct	gcg	ttc	ccg	cat	gct	gtt	gcc	ggt	ggt	ttt	336
Asn	Ser	Thr	Ala	Leu	Ala	Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe	
			100					105					110			
tta	aca	gct	gga	act	ttc	gtt	ctc	gga	att	tcg	ggt	tgg	tgg	att	att	384
Leu	Thr	Ala	Gly	Thr	Phe	Val	Leu	Gly	Ile	Ser	Gly	Trp	Trp	Ile	Ile	
		115				120						125				
cgt	gcg	cac	cgt	cag	gcc	aag	aag	gct	gag	tcg	gaa	atc	gag	tcg	aag	432
Arg	Ala	His	Arg	Gln	Ala	Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys	
	130					135					140					
cat	tcg	atg	cac	agg	ccc	gcg	ttg	tgg	gtt	ggt	tgg	tgg	acc	aca	gtt	480
His	Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val	
	145				150					155					160	
gtc	tct	tcc	gtg	gcg	ctg	ttc	atc	act	ggc	gat	atc	cag	gcg	aag	ctc	528
Val	Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu	
				165					170					175		
atg	ttc	gtg	caa	cag	cca	atg	aag	atg	gcg	tcg	gcg	gaa	tcc	ttg	tgt	576
Met	Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys	
		180					185						190			
gaa	acc	gcc	aca	gat	cca	aac	ttc	tcc	att	ctg	aca	att	ggt	acg	cac	624
Glu	Thr	Ala	Thr	Asp	Pro	Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His	
		195				200						205				
aac	aac	tgc	gat	acg	gta	acc	cac	ctg	atc	gat	gtt	ccg	ttt	gtg	ctt	672
Asn	Asn	Cys	Asp	Thr	Val	Thr	His	Leu	Ile	Asp	Val	Pro	Phe	Val	Leu	
	210					215					220					
cca	ttc	ttg	gct	gaa	gga	aaa	ttc	acc	ggt	gtg	act	ttg	cag	ggt	gta	720
Pro	Phe	Leu	Ala	Glu	Gly	Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val	
	225				230				235						240	
aac	cag	ctc	caa	gct	gca	gcg	gag	caa	gca	tac	ggt	cct	ggc	aac	tac	768
Asn	Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr	
			245						250					255		
tcc	cct	aac	ttg	ttt	gtc	acc	tac	tgg	tca	ttc	cgc	gca	atg	atc	ggc	816
Ser	Pro	Asn	Leu	Phe	Val	Thr	Tyr	Trp	Ser	Phe	Arg	Ala	Met	Ile	Gly	



260	265	270	
ctg atg ctt ggt tct ttg gct atc gct gcg att gcg tgg ctg ttg ctg			864
Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu			
275	280	285	
cgt aag aag cgc aca cca act gga aag att gct cgt ctg ttc cag atc			912
Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile			
290	295	300	
ggc agc ctc att gct atc ccg ttc cca ttc ttg gcc aac tct gct ggt			960
Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly			
305	310	315	320
tgg atc ttc acc gag atg ggc cgc cag cct tgg gtg gtg cac ccg aac			1008
Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn			
325	330	335	
cct gaa tct gcc ggc gat gcc cga aca gag atg atc cgg atg act gtt			1056
Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val			
340	345	350	
gat atg ggt gta tct gat cat gcg cca tgg caa gtc tgg ctg act ctc			1104
Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu			
355	360	365	
att ggc ttc acg att ctc tat ctc att ttg ttc gtg gtg tgg gtg tgg			1152
Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp			
370	375	380	
ctg att cgc cgc gca gtt ctg atc gga cca cca gag gaa ggc gct cca			1200
Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro			
385	390	395	400
tcc gtg gag gca aag act gga ccg gca acc ccg att ggt tca gat atg			1248
Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met			
405	410	415	
ccc atg aca ccg ctg caa ttt act gcc gct gcc cca acc aca ggt gaa			1296
Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu			
420	425	430	
aag gaa taaccatgga tctcaataacc ttt			1325
Lys Glu			

&lt;210&gt; 646

&lt;211&gt; 434

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 646

Trp Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu  
 1 5 10 15

Ala Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly  
 20 25 30

Leu Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala  
 35 40 45

Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile  
 50 55 60  
 Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn  
 65 70 75 80  
 Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr  
 85 90 95  
 Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe  
 100 105 110  
 Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile  
 115 120 125  
 Arg Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys  
 130 135 140  
 His Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val  
 145 150 155 160  
 Val Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu  
 165 170 175  
 Met Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys  
 180 185 190  
 Glu Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His  
 195 200 205  
 Asn Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu  
 210 215 220  
 Pro Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val  
 225 230 235 240  
 Asn Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr  
 245 250 255  
 Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly  
 260 265 270  
 Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu  
 275 280 285  
 Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile  
 290 295 300  
 Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly  
 305 310 315 320  
 Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn  
 325 330 335  
 Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val  
 340 345 350  
 Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu  
 355 360 365

Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp  
 370 375 380

Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro  
 385 390 395 400

Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met  
 405 410 415

Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu  
 420 425 430

Lys Glu

<210> 647  
 <211> 307  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(307)  
 <223> RXA00379

<400> 647  
 cggtgtggat aaacagcacc gccccgcagc agtgttcttg cgcaagtca cctccaaaga 60

tgtgttggat gttgcgttgc cattggtaga tgaggcctaa atg tct gag att gtg 115  
 Met Ser Glu Ile Val  
 1 5

gta gcc caa agc atc ggc cag cag ttt gct gac gtc gca gct tcc ggg 163  
 Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp Val Ala Ala Ser Gly  
 10 15 20

cca ctg ttc ctt ggc atc ctt gcc gca gcg ctc gca ggt ctg gtg tct 211  
 Pro Leu Phe Leu Gly Ile Leu Ala Ala Leu Ala Gly Leu Val Ser  
 25 30 35

ttt gcc agc ccg tgt gtt gtg ccg ttg gtg cca gga tat att tcc tac 259  
 Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro Gly Tyr Ile Ser Tyr  
 40 45 50

ctc gcc ggc gtg gtc ggt ggg gaa gtg gaa tac agc gct cat gcc acc 307  
 Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr Ser Ala His Ala Thr  
 55 60 65

<210> 648  
 <211> 69  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 648  
 Met Ser Glu Ile Val Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp  
 1 5 10 15

Val Ala Ala Ser Gly Pro Leu Phe Leu Gly Ile Leu Ala Ala Ala Leu  
 20 25 30

Ala Gly Leu Val Ser Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro  
 35 40 45

Gly Tyr Ile Ser Tyr Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr  
 50 55 60

Ser Ala His Ala Thr  
 65

<210> 649

<211> 362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(339)

<223> RXA00385

<400> 649

ctt ggc gga gtg ttc gct ctc ggt tgg acc cct tgt ttg ggc ccc acc 48  
 Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr  
 1 5 10 15

ctg gct gcg atc atc tcc att tct gca ggt act gaa ggc atg acc gct 96  
 Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala  
 20 25 30

gcg cgt ggc gtg atc tta att gtg ggt tac tgc ctc gga ctg ggg ctg 144  
 Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu  
 35 40 45

ccg ttc ctg ctg atc gcg ttg ggc tcc agc aag gca ctc acc gga gtc 192  
 Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val  
 50 55 60

gag tgg ttg cgc aag cat tcc cgc acc ctg caa att atc ggc ggt gtg 240  
 Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val  
 65 70 75 80

ttt ttg atc ttg gtc gga gta gcg ttg ctc tct ggc tca tgg gca att 288  
 Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile  
 85 90 95

ttt atc aac tgg gtc cgt cag tgg acc gtt gaa tac ggc gca aca ctg 336  
 Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu  
 100 105 110

ctc tagaaaaaga ctttttagtag gaa 362  
 Leu

<210> 650

<211> 113

<212> PRT

<213> Corynebacterium glutamicum

<400> 650

Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr  
 1 5 10 15  
 Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala  
 20 25 30  
 Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu  
 35 40 45  
 Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val  
 50 55 60  
 Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val  
 65 70 75 80  
 Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile  
 85 90 95  
 Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu  
 100 105 110

Leu

<210> 651  
 <211> 901  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(901)  
 <223> RXA01743

<400> 651  
 aggcaaagac tggaccggca accccgattg gttcagatat gcccatgaca ccgctgcaat 60  
 ttactgccgc tgccccaacc acaggtgaaa aggaataacc atg gat ctc aat acc 115  
 Met Asp Leu Asn Thr 5  
 1  
 ttt tgg ttt att ctc atc gca ttt ttg ttt gcg gga tac ttt ctc ctc 163  
 Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala Gly Tyr Phe Leu Leu 20  
 10 15  
 gaa gga ttc gac ttc ggc gtc gga att ttg gca ccc atc atc ggt aaa 211  
 Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala Pro Ile Ile Gly Lys 35  
 25 30  
 gat tca gcg gct agg aac aca gtg atc cgt acg att ggc cct gtc tgg 259  
 Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr Ile Gly Pro Val Trp 50  
 40 45  
 gac gga aat gaa gtg tgg ctg atc gtg gca ggt ggc gct ttg ttt gct 307  
 Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly Gly Ala Leu Phe Ala 65  
 55 60  
 gcc ttc cct gag tgg tac gca acg atg ttc tcc gga atg tat ctg ccg 355  
 Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser Gly Met Tyr Leu Pro 85  
 70 75 80

ctg ttc ctc gtg ctt gtg tcg ttg atc atg cgc gtg gtg ggc ctt gaa 403  
 Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg Val Val Gly Leu Glu  
                     90                    95                    100

tgg cgc aag aaa gtc gat gat cct cgt tgg caa aag tgg tct gac cgg 451  
 Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln Lys Trp Ser Asp Arg  
                     105                    110                    115

gcc atc ttt att ggt tct tgg act cca ccg ctg atg tgg gga ttc atc 499  
 Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu Met Trp Gly Phe Ile  
                     120                    125                    130

ttc gcc aat att ttg cgt ggc atg ccc ctc aag gcg gat cac acc atc 547  
 Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys Ala Asp His Thr Ile  
                     135                    140                    145

gat gct gcg gca gcc ctt cct ggc atg gtc aac gtc ttc gcc att ctg 595  
 Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn Val Phe Ala Ile Leu  
                     150                    155                    160                    165

ggt gca ctt gcg ttc acc gca ctg ttc gcc ctt cat ggt ctc gca ttc 643  
 Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu His Gly Leu Ala Phe  
                     170                    175                    180

atc cgc ctg aaa act gct ggt cgg gtg cgc acc gat gcg gcg aag gca 691  
 Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr Asp Ala Ala Lys Ala  
                     185                    190                    195

gct cca gta gtc gca ctt ctt gct gcg gtg act ggt gga cct ttc gtg 739  
 Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr Gly Gly Pro Phe Val  
                     200                    205                    210

ttg tgg gct gcc atc gca tac ggc cgt tcc tgg tcc tgg atc ctc gca 787  
 Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp Ser Trp Ile Leu Ala  
                     215                    220                    225

gtg ctg atc atc gca gcg gtt ctc ggt gga gct ttc gca ctg atc aaa 835  
 Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala Phe Ala Leu Ile Lys  
                     230                    235                    240                    245

gac cgc gat gga tta agc ttc ctg tcc act tcc gtc gct gtc atc ggt 883  
 Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser Val Ala Val Ile Gly  
                     250                    255                    260

gtc gtt gca ctg ctg ttt 901  
 Val Val Ala Leu Leu Phe  
                     265

&lt;210&gt; 652

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 652

Met Asp Leu Asn Thr Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala  
   1                    5                    10                    15

Gly Tyr Phe Leu Leu Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala  
           20                    25                    30

Pro Ile Ile Gly Lys Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr  
           35                          40                          45  
 Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly  
       50                          55                          60  
 Gly Ala Leu Phe Ala Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser  
   65                          70                          75                          80  
 Gly Met Tyr Leu Pro Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg  
                           85                          90                          95  
 Val Val Gly Leu Glu Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln  
                           100                          105                          110  
 Lys Trp Ser Asp Arg Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu  
           115                          120                          125  
 Met Trp Gly Phe Ile Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys  
   130                          135                          140  
 Ala Asp His Thr Ile Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn  
   145                          150                          155                          160  
 Val Phe Ala Ile Leu Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu  
                           165                          170                          175  
 His Gly Leu Ala Phe Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr  
                           180                          185                          190  
 Asp Ala Ala Lys Ala Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr  
                           195                          200                          205  
 Gly Gly Pro Phe Val Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp  
   210                          215                          220  
 Ser Trp Ile Leu Ala Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala  
   225                          230                          235                          240  
 Phe Ala Leu Ile Lys Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser  
                           245                          250                          255  
 Val Ala Val Ile Gly Val Val Ala Leu Leu Phe  
                           260                          265

&lt;210&gt; 653

&lt;211&gt; 1779

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1756)

&lt;223&gt; RXN02480

&lt;400&gt; 653

acctatgacc gctgtggcgc ctagggtcga cgggcacgtc gccctcaga ggcccagacc 60

gacaggccat gcacgcaagg gcagcaaagc atggttaatg atg acc acc acc gac 115

	Met	Thr	Thr	Thr	Asp	
	1				5	
cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttc						163
His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe						
	10		15		20	
ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc						211
Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr						
	25		30		35	
cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc						259
Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr						
	40		45		50	
atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg						307
Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp						
	55		60		65	
ggt ttt gct aac tac gtc ctg cca ctt cag atc ggt gcg cct gac gta						355
Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile Gly Ala Pro Asp Val						
	70		75		80	85
gct ttc cca cgt ttg aat gct ttc ggc ttc tgg atc acc acc gtc ggt						403
Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp Ile Thr Thr Val Gly						
	90		95		100	
ggt gtc gcg atg ctg acc ggc ttc ctg acc ccg ggt ggt gct gcc gac						451
Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro Gly Gly Ala Ala Asp						
	105		110		115	
ttc ggt tgg acc atg tac tcc cca ctg tct gac gca att cac tcc cca						499
Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp Ala Ile His Ser Pro						
	120		125		130	
ggc ctt ggc tct gac atg tgg att gtc ggt gtc ggt gca act ggt att						547
Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val Gly Ala Thr Gly Ile						
	135		140		145	
ggc tcc gtt gct tcc gca att aac atg ctc acc acc atc ctc tgc ctc						595
Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu						
	150		155		160	165
cgc gca cct ggt atg acc atg ttc cgt atg cct att ttc acc tgg aat						643
Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn						
	170		175		180	
atc ttc gtt gtt tcc gtt ctt gct ctg ctg atc ttc cca ctg ctg ctc						691
Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu						
	185		190		195	
gct gct gca ctg ggt gtt ctg tat gac cgc aag ctt ggt gga cac ctg						739
Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu						
	200		205		210	
tac gat cca gct aac ggc ggc tcc ctc ctg tgg cag cac ctg ttc tgg						787
Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp						
	215		220		225	
ttc ttc gga cac cct gag gtt tac gtt ctg gcg ctg ccg ttc ttc ggc						835
Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly						



230	235	240	245	
att gtt tct gag atc att cct gtg ttc tcc cgt aag cca atg ttc ggt Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly	250	255	260	883
tac gtc ggc ctg atc ttc gca acc ttg tcc att ggt gca ctg tcc atg Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile Gly Ala Leu Ser Met	265	270	275	931
gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt ttg ctt ccg Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val Leu Leu Pro	280	285	290	979
ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc ggc gtt aag Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr Gly Val Lys	295	300	305	1027
ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc act tgg gaa Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile Thr Trp Glu	310	315	320	1075
acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc ctc ttc ggt Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe Leu Phe Gly	330	335	340	1123
ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac ttc cac ttg Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp Phe His Leu	345	350	355	1171
gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc ctc ttc ggt Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr Leu Phe Gly	360	365	370	1219
acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg ttc ccg aag Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp Phe Pro Lys	375	380	385	1267
atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc cac ttc tgg Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile His Phe Trp	390	395	400	1315
ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag cac tgg gtg Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln His Trp Val	410	415	420	1363
ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg gat tct gat Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu Asp Ser Asp	425	430	435	1411
ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac ttc ctg ctt Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr Phe Leu Leu	440	445	450	1459
ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag tcc tgg cgc Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys Ser Trp Arg	455	460	465	1507
tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac ggc aac tcc Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr Gly Asn Ser	470	475	480	1555

ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac ttc gca tcc 1603  
 Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn Phe Ala Ser  
                     490                    495                    500

ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg cac tac ccg 1651  
 Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu His Tyr Pro  
                     505                    510                    515

cac atg att gaa cgc atg cgc gca gag gca cac act gga cat cac gat 1699  
 His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly His His Asp  
                     520                    525                    530

gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt gca tct gac 1747  
 Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu Ala Ser Asp  
                     535                    540                    545

tcc agc cgc taaaagcgtc tgatttaagt cgg 1779  
 Ser Ser Arg  
 550

<210> 654  
 <211> 552  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 654  
 Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met  
   1                    5                    10                    15  
 Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg  
                     20                    25                    30  
 Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe  
                     35                    40                    45  
 Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly  
                     50                    55                    60  
 Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile  
   65                    70                    75                    80  
 Gly Ala Pro Asp Val Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp  
                     85                    90                    95  
 Ile Thr Thr Val Gly Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro  
                     100                    105                    110  
 Gly Gly Ala Ala Asp Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp  
                     115                    120                    125  
 Ala Ile His Ser Pro Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val  
                     130                    135                    140  
 Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr  
   145                    150                    155                    160  
 Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro  
                     165                    170                    175

Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile  
 180 185 190  
 Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys  
 195 200 205  
 Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp  
 210 215 220  
 Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala  
 225 230 235 240  
 Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg  
 245 250 255  
 Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile  
 260 265 270  
 Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly  
 275 280 285  
 Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val  
 290 295 300  
 Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly  
 305 310 315 320  
 His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala  
 325 330 335  
 Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro  
 340 345 350  
 Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His  
 355 360 365  
 Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr  
 370 375 380  
 Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly  
 385 390 395 400  
 Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu  
 405 410 415  
 Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp  
 420 425 430  
 Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val  
 435 440 445  
 Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val  
 450 455 460  
 Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp  
 465 470 475 480  
 Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg  
 485 490 495  
 His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe

500 505 510  
 Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His  
 515 520 525  
 Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro  
 530 535 540  
 Ala Leu Ala Ser Asp Ser Ser Arg  
 545 550  
  
 <210> 655  
 <211> 385  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(385)  
 <223> FRXA01919  
  
 <400> 655  
 acctatgacc gctgtggcgc ctaggggtcga cgggcacgtc gcccctcaga ggcccagacc 60  
 gacaggccat gcacgcaagg gcagcaaagc atgggtaatg atg acc acc acc gac 115  
 Met Thr Thr Thr Asp  
 1 5  
 cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttt 163  
 His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe  
 10 15 20  
 ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211  
 Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr  
 25 30 35  
 cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259  
 Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr  
 40 45 50  
 atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307  
 Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp  
 55 60 65  
 ggt ttt gct aac tac gtc ctg cca ctt cca acc acc ang caa gcc ttc 355  
 Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr Thr Xaa Gln Ala Phe  
 70 75 80 85  
 tct aaa acc cgg gtg aac tct ccc agg gag 385  
 Ser Lys Thr Arg Val Asn Ser Pro Arg Glu  
 90 95  
  
 <210> 656  
 <211> 95  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 656  
 Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met

1	5	10	15
Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg	20	25	30
Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe	35	40	45
Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly	50	55	60
Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr	65	70	75
Thr Xaa Gln Ala Phe Ser Lys Thr Arg Val Asn Ser Pro Arg Glu	85	90	95

&lt;210&gt; 657

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(949)

&lt;223&gt; FRXA02480

&lt;400&gt; 657

tacgttctg cgtcgccgtt cttcggcatt gtttctgaga tcattcctgt gttctcccg 60

aagccaatgt tcgggttacg tcggcctgat cttcgcaacc ttg tcc att ggt gca	115
Leu Ser Ile Gly Ala	5
1	

ctg tcc atg gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt	163
Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val	20
10	15

ttg ctt ccg ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc	211
Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr	35
25	30

ggc gtt aag ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc	259
Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile	50
40	45

act tgg gaa acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc	307
Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe	65
55	60

ctc ttc ggt ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac	355
Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp	85
70	75

ttc cac ttg gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc	403
Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr	100
90	95

ctc ttc ggt acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg	451
Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp	

105	110	115	
ttc ccg aag atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc			499
Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile			
120	125	130	
cac ttc tgg ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag			547
His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln			
135	140	145	
cac tgg gtg ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg			595
His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu			
150	155	160	165
gat tct gat ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac			643
Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr			
170	175	180	
ttc ctg ctt ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag			691
Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys			
185	190	195	
tcc tgg cgc tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac			739
Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr			
200	205	210	
ggc aac tcc ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac			787
Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn			
215	220	225	
ttc gca tcc ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg			835
Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu			
230	235	240	245
cac tac ccg cac atg att gaa cgc atg cgc gca gag gca cac act gga			883
His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly			
250	255	260	
cat cac gat gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt			931
His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu			
265	270	275	
gca tct gac tcc agc cgc taaaagcgtc tgatttaagt cgg			972
Ala Ser Asp Ser Ser Arg			
280			

&lt;210&gt; 658

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 658

Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe  
 1 5 10 15

Val Thr Gly Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu  
 20 25 30

Ile Ser Val Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met  
 35 40 45

Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly  
     50                            55                            60  
 Phe Met Ala Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala  
     65                            70                            75                            80  
 Ser Pro Pro Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala  
                             85                            90                            95  
 His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala  
                             100                            105                            110  
 Gly Val Tyr Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu  
                             115                            120                            125  
 Arg Leu Gly Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly  
     130                            135                            140  
 Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg  
     145                            150                            155                            160  
 Tyr Ala Asp Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile  
                             165                            170                            175  
 Ser Thr Val Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile  
                             180                            185                            190  
 Trp Asn Val Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp  
     195                            200                            205  
 Asp Pro Trp Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro  
     210                            215                            220  
 Pro Pro Arg His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg  
     225                            230                            235                            240  
 Pro Ala Phe Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala  
                             245                            250                            255  
 Glu Ala His Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly  
                             260                            265                            270  
 Thr Ala Pro Ala Leu Ala Ser Asp Ser Ser Arg  
     275                            280

&lt;210&gt; 659

&lt;211&gt; 735

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(712)

&lt;223&gt; FRXA02481

&lt;400&gt; 659

tgctaactac gtcctgccac ttcagatcgg tgcgcctgac gtagctttcc cacgttgaaa 60

tgctttcggc ttctgaatca ccaccgtcgg tgggtgcgcg atg ctg acc ggc ttc 115

	Met	Leu	Thr	Gly	Phe	
	1				5	
cta acc ccg ggt ggt gct gcc gac ttg ggt gga cca tgt act ccc cac						163
Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly Pro Cys Thr Pro His						
				10	15	20
tgt ctg acg caa ttc act ccc cag gcc ttg gtt cta aca tgt gga ttg						211
Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val Leu Thr Cys Gly Leu						
				25	30	35
tcg ggt gtc ggt gca act ggt att ggc tcc gtt gct tcc gca att aac						259
Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn						
				40	45	50
atg ctc acc acc atc ctc tgc ctc cgc gca cct ggt atg acc atg ttc						307
Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe						
				55	60	65
cgt atg cct att ttc acc tgg aat atc ttc gtt gtt tcc gtt ctt gct						355
Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala						
				70	75	80
ctg ctg atc ttc cca ctg ctg ctc gct gct gca ctg ggt gtt ctg tat						403
Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr						
				90	95	100
gac cgc aag ctt ggt gga cac ctg tac gat cca gct aac ggc ggc tcc						451
Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser						
				105	110	115
ctc ctg tgg cag cac ctg ttc tgg ttc ttc gga cac cct gag gtt tac						499
Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr						
				120	125	130
gtt ctg gcg ctg ccg ttc ttc ggc att gtt tct gag atc att cct gtg						547
Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val						
				135	140	145
ttc tcc cgt aag cca atg ttc ggg tta cgt cgg cct gat ctt cgc aac						595
Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg Pro Asp Leu Arg Asn						
				150	155	160
ctt gtc cat tgg tgc act gtc cat ggc tgt gtg ggc tca cca cat gtt						643
Leu Val His Trp Cys Thr Val His Gly Cys Val Gly Ser Pro His Val						
				170	175	180
cgt tac tgg cgc agt ttt gct tcc gtt ctt ctc ctt cat gac gtt cct						691
Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu Leu His Asp Val Pro						
				185	190	195
gat ttc ggt tcc tac cgg cgt taagttcttc aactgggttg gaa						735
Asp Phe Gly Ser Tyr Arg Arg						
				200		

&lt;210&gt; 660

&lt;211&gt; 204

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 660

Met Leu Thr Gly Phe Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly  
 1 5 10 15

Pro Cys Thr Pro His Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val  
 20 25 30

Leu Thr Cys Gly Leu Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val  
 35 40 45

Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro  
 50 55 60

Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val  
 65 70 75 80

Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala  
 85 90 95

Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro  
 100 105 110

Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly  
 115 120 125

His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser  
 130 135 140

Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg  
 145 150 155 160

Pro Asp Leu Arg Asn Leu Val His Trp Cys Thr Val His Gly Cys Val  
 165 170 175

Gly Ser Pro His Val Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu  
 180 185 190

Leu His Asp Val Pro Asp Phe Gly Ser Tyr Arg Arg  
 195 200

&lt;210&gt; 661

&lt;211&gt; 1200

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1177)

&lt;223&gt; RXA02140

&lt;400&gt; 661

aacacaagat atggaatcgg ctggcaaata ggctattctg cgaagataga aatgaccgta 60

aggtctctgg tttttgtgtg gacaggaagg cagaacacac gtg gaa cag caa aat 115  
 Val Glu Gln Gln Asn  
 1 5

aag cgt ggt tta aag cgc aag gcc ctg ctt ggc ggt gtc ttg ggc tta 163  
 Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly Gly Val Leu Gly Leu  
 10 15 20

ggt ggc ctc gcc atg gca ggc tgt gaa gtc gcc cct cct ggc ggt gtg 211  
 Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala Pro Pro Gly Gly Val  
                   25                                  30                                  35

ctt gga gat ttc cta cgt atg ggt tgg cct gat ggc att acc cct gaa 259  
 Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp Gly Ile Thr Pro Glu  
                   40                                  45                                  50

gca gtg gcc atg ggt aac ttc tgg tca tgg gtc tgg gtt gct gcc tgg 307  
 Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val Trp Val Ala Ala Trp  
                   55                                  60                                  65

atc atc ggc atc atc atg tgg ggt cta ttc ctc acc gcc atc ttt gcc 355  
 Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu Thr Ala Ile Phe Ala  
                   70                                  75                                  80                                  85

tgg ggc gca aag agg gct gaa aag cgc ggc gag ggt gaa ttc cct aag 403  
 Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu Gly Glu Phe Pro Lys  
                                   90                                  95                                  100

cag ctc cag tac aac gtt cca ctt gag ctc gtt ctg acg atc gtt ccg 451  
 Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val Leu Thr Ile Val Pro  
                   105                                  110                                  115

atc atc att gtt atg gtg ctg ttc ttc ttc acc gtt caa act cag gac 499  
 Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr Val Gln Thr Gln Asp  
                   120                                  125                                  130

aag gtc acc gct ctg gat aag aac cca gag gtt acc gtg gac gtc acc 547  
 Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val Thr Val Asp Val Thr  
                   135                                  140                                  145

gct tac cag tgg aac tgg aag ttc gga tac tcc gaa att gat ggc tca 595  
 Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser Glu Ile Asp Gly Ser  
                   150                                  155                                  160                                  165

ctg gca cct ggt gga cag gat tac caa gga agc gac ccg gag cgt cag 643  
 Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser Asp Pro Glu Arg Gln  
                                   170                                  175                                  180

gca gct gcc gag gct tcc aag aag gat cct tct gga gat aac cca att 691  
 Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser Gly Asp Asn Pro Ile  
                   185                                  190                                  195

cac ggc aac tca aag tct gac gtt tct tac ctt gag ttc aac cga att 739  
 His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu Glu Phe Asn Arg Ile  
                   200                                  205                                  210

gaa acc ctc gga acc act gat gaa atc cca gtg atg gtt ctt cct gtg 787  
 Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val Met Val Leu Pro Val  
                   215                                  220                                  225

aac acc cca atc gag ttc aac ctc gca tct gct gac gtt gca cac tcc 835  
 Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala Asp Val Ala His Ser  
                   230                                  235                                  240                                  245

ttc tgg gtt cca gag ttc ctc ttc aag cga gat gct tac gca cac cct 883  
 Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp Ala Tyr Ala His Pro  
                                   250                                  255                                  260

gag gca aac aag tcc cag cgt gtc ttc cag att gaa gag atc act gag 931  
Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile Glu Glu Ile Thr Glu  
265 270 275

gaa ggc gca ttc gtt ggt cgc tgt gca gaa atg tgc ggt act tac cac 979  
Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met Cys Gly Thr Tyr His  
280 285 290

gca atg atg aac ttc gag ctt cgt gtc gtc gat cgc gat tcc ttc gct 1027  
Ala Met Met Asn Phe Glu Leu Arg Val Val Asp Arg Asp Ser Phe Ala  
295 300 305

gag tac atc agc ttc cgt gac tcc aac cca gac gca acc aac gct cag 1075  
Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp Ala Thr Asn Ala Gln  
310 315 320 325

gca ctt gag cac att ggt caa gct cct tac gct act tcc act agc cca 1123  
Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala Thr Ser Thr Ser Pro  
330 335 340

ttc gtt tcc gat cgc acc gca acc cgc gac ggc gaa aac act cag agc 1171  
Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly Glu Asn Thr Gln Ser  
345 350 355

aac gct taagaaggag tggcgaaaaa atg 1200  
Asn Ala

<210> 662

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 662

Val Glu Gln Gln Asn Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly  
1 5 10 15

Gly Val Leu Gly Leu Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala  
20 25 30

Pro Pro Gly Gly Val Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp  
35 40 45

Gly Ile Thr Pro Glu Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val  
50 55 60

Trp Val Ala Ala Trp Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu  
65 70 75 80

Thr Ala Ile Phe Ala Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu  
85 90 95

Gly Glu Phe Pro Lys Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val  
100 105 110

Leu Thr Ile Val Pro Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr  
115 120 125

Val	Gln	Thr	Gln	Asp	Lys	Val	Thr	Ala	Leu	Asp	Lys	Asn	Pro	Glu	Val
130						135					140				

Thr Val Asp Val Thr Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser  
 145 150 155 160  
 Glu Ile Asp Gly Ser Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser  
 165 170 175  
 Asp Pro Glu Arg Gln Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser  
 180 185 190  
 Gly Asp Asn Pro Ile His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu  
 195 200 205  
 Glu Phe Asn Arg Ile Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val  
 210 215 220  
 Met Val Leu Pro Val Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala  
 225 230 235 240  
 Asp Val Ala His Ser Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp  
 245 250 255  
 Ala Tyr Ala His Pro Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile  
 260 265 270  
 Glu Glu Ile Thr Glu Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met  
 275 280 285  
 Cys Gly Thr Tyr His Ala Met Met Asn Phe Glu Leu Arg Val Val Asp  
 290 295 300  
 Arg Asp Ser Phe Ala Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp  
 305 310 315 320  
 Ala Thr Asn Ala Gln Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala  
 325 330 335  
 Thr Ser Thr Ser Pro Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly  
 340 345 350  
 Glu Asn Thr Gln Ser Asn Ala  
 355  
  
 <210> 663  
 <211> 774  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(751)  
 <223> RXA02142  
  
 <400> 663  
 acgaaaagtt cccggaaggt cgattgaaaa gtttgcaaat tgggggaaaa ttgcacatcaa 60  
 aagccgagtt caaaccttca attgaaacgg ggggcttgaa gtg act ttg gcc aac 115  
 Val Thr Leu Ala Asn  
 1 5

caa aca gcc ata cta gat agc gtg acg agc gca gtt gga aat aca ggt	163
Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala Val Gly Asn Thr Gly	
10 15 20	
atg gca gca cca caa cgt gtt gcg gca ctg aac cgt ccg aat atg gtc	211
Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn Arg Pro Asn Met Val	
25 30 35	
agt gtc ggc acc att gtg ttc ctg tct cag gaa tta atg ttc ttc gcc	259
Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu Leu Met Phe Phe Ala	
40 45 50	
ggg cta ttc gcg atg tac ttc gtg tcc cgt gcg aac gga ctg gca aat	307
Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala Asn Gly Leu Ala Asn	
55 60 65	
gga tca tgg gga gag cag aca gat cac ctc aac gtg ccc tac gca ctg	355
Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn Val Pro Tyr Ala Leu	
70 75 80 85	
ttg att acg gtc att ctg gtg tct tcc tca gtg act tgc cag ttc gga	403
Leu Ile Thr Val Ile Leu Val Ser Ser Val Thr Cys Gln Phe Gly	
90 95 100	
gtt ttt gcg gct gaa agg ggt gac gtt tac ggc ctc cgc aag tgg ttc	451
Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly Leu Arg Lys Trp Phe	
105 110 115	
ttg gtc acg att atc ctc gga tca atc ttc gtg atc gga'cag ggc tac	499
Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val Ile Gly Gln Gly Tyr	
120 125 130	
gag tac atc act ctc gta ggt cac gga ctt aca atc cag agc agt gtc	547
Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr Ile Gln Ser Ser Val	
135 140 145	
tac gga tcg gca ttc ttt att aca acc ggt ttc cac gca ctg cac gtg	595
Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe His Ala Leu His Val	
150 155 160 165	
atc gcg ggt gtt atg gcc ttc gtt gtg gtt ctt atg aga atc cat aag	643
Ile Ala Gly Val Met Ala Phe Val Val Val Leu Met Arg Ile His Lys	
170 175 180	
tcg aag ttc act ccg gca cag gca acc gca gca atg gtt gtg tct tat	691
Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala Met Val Val Ser Tyr	
185 190 195	
tac tgg cac ttc gtt gac gtg gtc tgg atc ggc ctc ttc atc act att	739
Tyr Trp His Phe Val Asp Val Val Trp Ile Gly Leu Phe Ile Thr Ile	
200 205 210	
tac ttc att cag taggcagtaa ggaatcctca acg	774
Tyr Phe Ile Gln	
215	

&lt;210&gt; 664

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 664

Val Thr Leu Ala Asn Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala  
 1 5 10 15  
 Val Gly Asn Thr Gly Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn  
 20 25 30  
 Arg Pro Asn Met Val Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu  
 35 40 45  
 Leu Met Phe Phe Ala Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala  
 50 55 60  
 Asn Gly Leu Ala Asn Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn  
 65 70 75 80  
 Val Pro Tyr Ala Leu Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val  
 85 90 95  
 Thr Cys Gln Phe Gly Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly  
 100 105 110  
 Leu Arg Lys Trp Phe Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val  
 115 120 125  
 Ile Gly Gln Gly Tyr Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr  
 130 135 140  
 Ile Gln Ser Ser Val Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe  
 145 150 155 160  
 His Ala Leu His Val Ile Ala Gly Val Met Ala Phe Val Val Val Leu  
 165 170 175  
 Met Arg Ile His Lys Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala  
 180 185 190  
 Met Val Val Ser Tyr Tyr Trp His Phe Val Asp Val Val Trp Ile Gly  
 195 200 205  
 Leu Phe Ile Thr Ile Tyr Phe Ile Gln  
 210 215

&lt;210&gt; 665

&lt;211&gt; 1347

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1324)

&lt;223&gt; RXA02144

&lt;400&gt; 665

actcactcgg tagcttgggc ccagtggctg agggctctgtt catgtgggta ttcggcatct 60

tggtcctcgt ggccgcccgt atgtggattg gatcacgttc atg agt aac aac aac 115  
 Met Ser Asn Asn Asn  
 1 5

gac aaa cag tac aca acc caa gaa ctc aac gcg atg agc aat gag gat	163
Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala Met Ser Asn Glu Asp	
10 15 20	
ctt gca cga ctt ggt aca gag ctg gac gac gtt acc att gca tac cgc	211
Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val Thr Ile Ala Tyr Arg	
25 30 35	
aag gaa cgt ttc cca atc gct aat gac cca gct gag aag cgc gct gca	259
Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala Glu Lys Arg Ala Ala	
40 45 50	
cgt gca gtt act ttc tgg cta gtc ctc ggc atc att ggt gga ctt ggg	307
Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile Ile Gly Gly Leu Gly	
55 60 65	
ttc ctg gct acc tac att ttc tgg cct tgg gag tac aag gca cac gga	355
Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu Tyr Lys Ala His Gly	
70 75 80 85	
gat gaa ggt ctc ctg gcg tac acc ttg tac acc cca atg ctg ggt att	403
Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr Pro Met Leu Gly Ile	
90 95 100	
act tcc ggt ctt tgc atc ctg tcc ctg gga ttt gca gtt gtc ctt tat	451
Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe Ala Val Val Leu Tyr	
105 110 115	
gtc aag aag ttc att cca gag gaa atc gca gta cag cgt cgc cac gac	499
Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val Gln Arg Arg His Asp	
120 125 130	
ggt cct tct gaa gaa gtt gac cgc cgc acc atc gtt gca ctt ctc aat	547
Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile Val Ala Leu Leu Asn	
135 140 145	
gac tct tgg cag acc tct act ctt ggt cgt cgc aag ctg atc atg gga	595
Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg Lys Leu Ile Met Gly	
150 155 160 165	
ctt gca ggt ggc gga gca gta ctg gcc ggc ctg acc atc atc gct cca	643
Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu Thr Ile Ile Ala Pro	
170 175 180	
atg ggc ggt atg atc aag aac cct tgg aat cct aag gaa ggc cca atg	691
Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro Lys Glu Gly Pro Met	
185 190 195	
gac gtt cag ggt gac ggc acc ctg tgg act tcc ggt tgg act ctc gtt	739
Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser Gly Trp Thr Leu Val	
200 205 210	
gag aac gac gtc aag gtt tac ctc ggc cgc gac act gca gca att gcg	787
Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp Thr Ala Ala Ile Ala	
215 220 225	
gag tcc cac acc gat gca acc ggt gag cac tgg tca acc act ggt gtt	835
Glu Ser His Thr Asp Ala Thr Gly Glu His Trp Ser Thr Thr Gly Val	
230 235 240 245	

```
<210> 666
<211> 408
<212> PRT
<213> Corynebacterium glutamicum
```

946



50	55	60
Ile Gly Gly Leu Gly Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu 65 70 75 80		
Tyr Lys Ala His Gly Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr 85 90 95		
Pro Met Leu Gly Ile Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe 100 105 110		
Ala Val Val Leu Tyr Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val 115 120 125		
Gln Arg Arg His Asp Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile 130 135 140		
Val Ala Leu Leu Asn Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg 145 150 155 160		
Lys Leu Ile Met Gly Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu 165 170 175		
Thr Ile Ile Ala Pro Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro 180 185 190		
Lys Glu Gly Pro Met Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser 195 200 205		
Gly Trp Thr Leu Val Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp 210 215 220		
Thr Ala Ala Ile Ala Glu Ser His Thr Asp Ala Thr Gly Glu His Trp 225 230 235 240		
Ser Thr Thr Gly Val Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu 245 250 255		
Ala Ala Ala Ser Met Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val 260 265 270		
Asn Asp Gly Ala Glu Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln 275 280 285		
Met His Ser Val His Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu 290 295 300		
Arg Thr Ala Asp Ala Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser 305 310 315 320		
Phe His Tyr Gly Asp Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile 325 330 335		
Gly Cys Pro Thr Ser Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys 340 345 350		
Pro Cys His Gln Ser Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val 355 360 365		
Phe Gly Pro Ala Ala Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp 370 375 380		

Glu Glu Gly Tyr Leu Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly  
 385 390 395 400

Pro Ala Phe Trp Glu Arg Lys Ser  
 405

<210> 667

<211> 1053

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1030)

<223> RXA02740

<400> 667

aacgcaaggt gcacactcac cgcaggggata tttaaataat aaggactcac aacttaaata 60

tatgagtgat ttgaaaatgc aacgttctgg aggagaaccc ttg gac acg atc aag 115  
 Leu Asp Thr Ile Lys  
 1 5

gcc tat att gcg cta acg aag ccc agg gtt att gaa ctc ctc ctt gtc 163  
 Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile Glu Leu Leu Leu Val  
 10 15 20

gcc aca atc ccc aca atg ctt cag gct gaa cgc ggt gag aac aac att 211  
 Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg Gly Glu Asn Asn Ile  
 25 30 35

gtg ctc atc ttg ctg act gtg ttc ggt ggc tgg atg ggt gcg gcc gcc 259  
 Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp Met Gly Ala Ala Ala  
 40 45 50

gcc aac acc ttc aac atg gtg gca gac tcc gat att gat cag cgc atg 307  
 Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp Ile Asp Gln Arg Met  
 55 60 65

gga cgc act agg gct cgc cct ttg gtg cgc cac acc gtg agt aat cgc 355  
 Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His Thr Val Ser Asn Arg  
 70 75 80 85

gac gcc tcc att ttt gcg tgg gtc ctg aca gtg gcc agc ttc ttg tgg 403  
 Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val Ala Ser Phe Leu Trp  
 90 95 100

ctg tgg ctg ctg tgc gat tcg atg ctc gcc ggc atc ttc gtg ttg atc 451  
 Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly Ile Phe Val Leu Ile  
 105 110 115

acg att ttc ttc tac att ttt gtc tac acc aag tgg ctg aag cgc cgc 499  
 Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys Trp Leu Lys Arg Arg  
 120 125 130

acg cac atg aat atc gtg tgg ggc gga gcc gca ggt tgt atg cca gtg 547  
 Thr His Met Asn Ile Val Trp Gly Gly Ala Ala Gly Cys Met Pro Val  
 135 140 145

ctc gtc ggc tgg gca gtg atc gtt gat cag ttt gag cca ggc gtt cca 595  
 Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe Glu Pro Gly Val Pro  
 150 155 160 165

cag cag tgg tgg cag gca att gtc ctg ttc atg gtg att ttc ttc tgg 643  
 Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met Val Ile Phe Phe Trp  
 170 175 180

acc cca cct cac acc tgg gct ctg gcc atg aag tac cgc gaa gac tac 691  
 Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys Tyr Arg Glu Asp Tyr  
 185 190 195

aag gcg gct ggc gtc cca atg ctt cct gtc gtg cgc acc cca gtc cag 739  
 Lys Ala Ala Gly Val Pro Met Leu Pro Val Val Arg Thr Pro Val Gln  
 200 205 210

gtc acc gca caa atc gtg tgg tac tcc gtg gca act gtg ctg acc acc 787  
 Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala Thr Val Leu Thr Thr  
 215 220 225

ttc ttg ctc atc cca gca act ggt tgg atc tac gca gcg atc gcc gtc 835  
 Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr Ala Ala Ile Ala Val  
 230 235 240 245

att tcc ggc gtc acc ttc ttg ttc atg gcc atc aag ctg cac ctc ggc 883  
 Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile Lys Leu His Leu Gly  
 250 255 260

atc aaa aac ggt ggc aag gtc aag cct ctg aag ctg ttt att ttg tcc 931  
 Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys Leu Phe Ile Leu Ser  
 265 270 275

aac aac tac ttg gca gtc ctc ttc gtg gca ttg tcc gtc gac gcg gtc 979  
 Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu Ser Val Asp Ala Val  
 280 285 290

ctc ggc ctt gag acc atc ggc gag atg ctc ggc tgg acc acc acc ttc 1027  
 Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly Trp Thr Thr Thr Phe  
 295 300 305

ttc taaaagcttg cttttcgacg aaa 1053  
 Phe  
 310

&lt;210&gt; 668

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 668

Leu Asp Thr Ile Lys Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile  
 1 5 10 15

Glu Leu Leu Leu Val Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg  
 20 25 30

Gly Glu Asn Asn Ile Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp  
 35 40 45

Met Gly Ala Ala Ala Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp

50	55	60
Ile Asp Gln Arg Met Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His 65 70 75 80		
Thr Val Ser Asn Arg Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val 85 90 95		
Ala Ser Phe Leu Trp Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly 100 105 110		
Ile Phe Val Leu Ile Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys 115 120 125		
Trp Leu Lys Arg Arg Thr His Met Asn Ile Val Trp Gly Gly Ala Ala 130 135 140		
Gly Cys Met Pro Val Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe 145 150 155 160		
Glu Pro Gly Val Pro Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met 165 170 175		
Val Ile Phe Phe Trp Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys 180 185 190		
Tyr Arg Glu Asp Tyr Lys Ala Ala Gly Val Pro Met Leu Pro Val Val 195 200 205		
Arg Thr Pro Val Gln Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala 210 215 220		
Thr Val Leu Thr Thr Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr 225 230 235 240		
Ala Ala Ile Ala Val Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile 245 250 255		
Lys Leu His Leu Gly Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys 260 265 270		
Leu Phe Ile Leu Ser Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu 275 280 285		
Ser Val Asp Ala Val Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly 290 295 300		
Trp Thr Thr Thr Phe Phe 305 310		

&lt;210&gt; 669

&lt;211&gt; 1161

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1138)

&lt;223&gt; RXA02743

<400> 669

atataccttaaa aagtttcccgaggagttttcagtg ggcacaataacc accactttcca taccgggaac															60
aattgtataaa aactagccat gacctgctag gatcagcgac															115
Val Ser Thr Ser Asp															15
gct ccc tca aat aat cca gtt gag ttg aag ccc att act ttc tgg gca															163
Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala															20
ccg acc atc aaa gtg cag cgc att ctc gcg ctc cta ctg ttg att ttc															211
Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu Leu Leu Ile Phe															35
cag gga ggc atc acc gtt acg ggc tct atc gtc cgt gtc aca ggc tcc															259
Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val Arg Val Thr Gly Ser															40
ggc ctc ggt tgt gat acc tgg cca cta tgc cac gaa ggt tca cta gtc															307
Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His Glu Gly Ser Leu Val															55
cca gtc gca ggc gca gca cca tgg atc cac cag gca gtg gaa ttt ggt															355
Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln Ala Val Glu Phe Gly															70
aac cgc atg ctc act ttc gtg ctt gct gcc gca gcg ctt gcg ttg ttc															403
Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala Leu Ala Leu Phe															90
att gca gtt ctt ggc gca aaa cgc cgc cgc gag atc ctg gtc cat tcc															451
Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu Ile Leu Val His Ser															105
ttc atc cag ggt ttg ggc atc atc ttg cag gct gtc atc ggt ggc atc															499
Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala Val Ile Gly Gly Ile															120
acc gtg ctg gtt gat ttg cac tgg tac gcc gtt gct ttg cac ttc ctg															547
Thr Val Leu Val Asp Leu His Trp Tyr Ala Val Ala Leu His Phe Leu															135
cca tcc atg atc ctt gtt ttc atg gcc gcg att ttg tac acc cgc atc															595
Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile Leu Tyr Thr Arg Ile															150
ggc gag ccc gat gac ggc gag att acc acc aca ttc ccc acg tgg atc															643
Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr Phe Pro Thr Trp Ile															170
cgc aat gta gct gtc att ggt gca gta gcg ctc tcc gta gta ctg atc															691
Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu Ser Val Val Leu Ile															185
acc ggc acc atg acc acc ggc gct ggc gtt cac tct ggc gat gca tca															739
Thr Gly Thr Met Thr Thr Gly Ala Gly Val His Ser Gly Asp Ala Ser															200
atc acc atg gat gat cgc ctc gat gtc agc atc gac ttg atg gcc cac															787
Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile Asp Leu Met Ala His															

215                      220                      225  
 atc cac ggc tac agc atg tac atc tac ctc ttc ttc acc ctc atc gtg 835  
 Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe Phe Thr Leu Ile Val  
 230                      235                      240                      245  
 gtc gcc ggt ctg tac aag gca aaa acc acc aag cac aac aag cag ctt 883  
 Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys His Asn Lys Gln Leu  
 250                      255                      260  
 ggc ctc atg ctg att ctg ttc att ctg att cag gca ggt atc ggc atc 931  
 Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln Ala Gly Ile Gly Ile  
 265                      270                      275  
 ttg cag tac cgc atg ggt gtg cca cgc tgg agc atc cca ttc cac atc 979  
 Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser Ile Pro Phe His Ile  
 280                      285                      290  
 gca atg tct tct gtc gtt gtt gcc ttc act tcc ctt ctg tgg gcg cag 1027  
 Ala Met Ser Ser Val Val Val Ala Phe Thr Ser Leu Leu Trp Ala Gln  
 295                      300                      305  
 ggt cgt ata cgc gtc ggc ggt aaa gcc acc gtt act ggt tct gtt gat 1075  
 Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val Thr Gly Ser Val Asp  
 310                      315                      320                      325  
 ggc gat att aag aac gag atc att acg aac ccc ttt gag aag aaa tca 1123  
 Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser  
 330                      335                      340  
 aag cag cct gtt aaa taacacgcaa ctgtatcggt aaa 1161  
 Lys Gln Pro Val Lys  
 345  
  
 <210> 670  
 <211> 346  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 670  
 Val Ser Thr Ser Asp Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro  
 1                      5                      10                      15  
 Ile Thr Phe Trp Ala Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu  
 20                      25                      30  
 Leu Leu Leu Ile Phe Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val  
 35                      40                      45  
 Arg Val Thr Gly Ser Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His  
 50                      55                      60  
 Glu Gly Ser Leu Val Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln  
 65                      70                      75                      80  
 Ala Val Glu Phe Gly Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala  
 85                      90                      95  
 Ala Leu Ala Leu Phe Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu  
 100                      105                      110

Ile Leu Val His Ser Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala  
 115 120 125  
 Val Ile Gly Gly Ile Thr Val Leu Val Asp Leu His Trp Tyr Ala Val  
 130 135 140  
 Ala Leu His Phe Leu Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile  
 145 150 155 160  
 Leu Tyr Thr Arg Ile Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr  
 165 170 175  
 Phe Pro Thr Trp Ile Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu  
 180 185 190  
 Ser Val Val Leu Ile Thr Gly Thr Met Thr Thr Gly Ala Gly Val His  
 195 200 205  
 Ser Gly Asp Ala Ser Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile  
 210 215 220  
 Asp Leu Met Ala His Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe  
 225 230 235 240  
 Phe Thr Leu Ile Val Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys  
 245 250 255  
 His Asn Lys Gln Leu Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln  
 260 265 270  
 Ala Gly Ile Gly Ile Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser  
 275 280 285  
 Ile Pro Phe His Ile Ala Met Ser Ser Val Val Val Ala Phe Thr Ser  
 290 295 300  
 Leu Leu Trp Ala Gln Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val  
 305 310 315 320  
 Thr Gly Ser Val Asp Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro  
 325 330 335  
 Phe Glu Lys Lys Ser Lys Gln Pro Val Lys  
 340 345

&lt;210&gt; 671

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(421)

&lt;223&gt; RXA01227

&lt;400&gt; 671

ggataatcga aaatatgtgc cccttggtga agggtcgggg agctaataagg atgacagtga 60

acctatttttc cacgtcttta tccgtagtat tggagatccg atg acc tac aca atc 115

	Met	Thr	Tyr	Thr	Ile	
	1				5	
gcc cag ccc tgc gtt gat gtc ctg gat cga gcc tgc gtc gag gaa tgt						163
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys						
	10				20	
ccc gtg gac tgc atc tac gag ggc aaa cgg atg ctc tac atc cac ccc						211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro						
	25				35	
gat gag tgc gtc gac tgc ggt gcc tgc gag ccc gtc tgc ccg gtt gaa						259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Val Cys Pro Val Glu						
	40				50	
gcc atc ttc tac gaa gat gat gtt ccc cac gaa tgg tgg gac tac acc						307
Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu Trp Trp Asp Tyr Thr						
	55				65	
ggc gct aac gcc gcc ttt ttc gac gac ctc ggt tcg cca ggc ggt gcc						355
Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala						
	70				80	85
gcc agc ctg ggt ccg cag gac ttc gac gcc cag ctc gtc gcg gtg ctg						403
Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln Leu Val Ala Val Leu						
	90				95	100
ccg cca cag aac cag aac taggacctga tatcgccct aaa						444
Pro Pro Gln Asn Gln Asn						
	105					

&lt;210&gt; 672

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 672

Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala									
1				5			10		15
Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met									
	20				25			30	
Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro									
	35				40			45	
Val Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu									
	50				55			60	
Trp Trp Asp Tyr Thr Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly									
	65				70			75	80
Ser Pro Gly Gly Ala Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln									
	85				90			95	
Leu Val Ala Val Leu Pro Pro Gln Asn Gln Asn									
	100							105	

&lt;210&gt; 673



```
<211> 438
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(415)  
<223> RXA01865
```

[illegible]

```
<210> 674
<211> 105
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 674
Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala
  1             5             10             15

Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
          20             25             30

Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
      35             40             45

Ala Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu

```



&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 676

Met Ser Thr Ile His Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile  
 1 5 10 15

Glu Ala Thr Val Gly Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly  
 20 25 30

Val Pro Gly Ile Val Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr  
 35 40 45

Cys His Val Phe Val Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met  
 50 55 60

Glu Glu Met Glu Asp Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu  
 65 70 75 80

Asp Cys Ser Arg Leu Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp  
 85 90 95

Leu Ser Leu Thr Thr Pro Glu Thr Gln Val  
 100 105

&lt;210&gt; 677

&lt;211&gt; 1389

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1366)

&lt;223&gt; RXA00679

&lt;400&gt; 677

ggaccgtgag gattgctccc gtttgtcttg ccaaatacaag gtcaccgaag gcatggatct 60

ttcgttgacc acgccagaaa cgcaagtgtg aggttgaatc atg aat act tca gct 115  
 Met Asn Thr Ser Ala  
 1 5

gaa act gga atc ttg atc atc ggt gca aac caa tcg ggt gtg cag ctg 163  
 Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln Ser Gly Val Gln Leu  
 10 15 20

gcg att tcc ctg cgg gcc acg ggt ttc acc gaa tcg atc acg ctt cta 211  
 Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu Ser Ile Thr Leu Leu  
 25 30 35

ggc gag gag gat cac cgc ccc tac cag cgt ccc gcc ttg tcc aag gag 259  
 Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro Ala Leu Ser Lys Glu  
 40 45 50

ttc ctc cag gac aag atc gac aaa gag cgt ctg att ttc cgt tcc aat 307  
 Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu Ile Phe Arg Ser Asn  
 55 60 65

gag tat tgg gaa gaa aat aat att cgc ctg gtc aag ggc gtg cgc atc 355  
 Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val Lys Gly Val Arg Ile  
 70 75 80 85

gaa cgc att gaa aag aac gac gac gga tca ggg gtc gcc tac ggc gcc	403
Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly Val Ala Tyr Gly Ala	
90 95 100	
gga caa gaa ttc gct ttt cga cgt ctc gct cta gcg gtt ggt gcc cgc	451
Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu Ala Val Gly Ala Arg	
105 110 115	
cct cgc cac ctc gac ctc ccg ggc gcc acc ttg gag ggt gtc acc tac	499
Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu Glu Gly Val Thr Tyr	
120 125 130	
ctg cgc aac gcg gac gac gcc ttg gcg ctc aaa gcg atg att ggt tct	547
Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys Ala Met Ile Gly Ser	
135 140 145	
gtc acc gat gcc gtt gta gtc ggt ggt ggg ttc atc gga ttg gaa gct	595
Val Thr Asp Ala Val Val Val Gly Gly Gly Phe Ile Gly Leu Glu Ala	
150 155 160 165	
gcg tgt tcg ctt cat gac ctc ggc aaa aat gtc acc gtc ctg gaa tat	643
Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val Thr Val Leu Glu Tyr	
170 175 180	
ggt ccg cgt ctg att ggc cga gcg gtg ggt gaa gaa acc gca gca ttc	691
Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu Glu Thr Ala Ala Phe	
185 190 195	
ttc ctc gaa caa cac cgt tcc cgt ggc gta aat atc gtg ctt gat gcc	739
Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn Ile Val Leu Asp Ala	
200 205 210	
cgc atg aaa cag ttt gtg ggc aag gat gga aag ctc agc ggc att gag	787
Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys Leu Ser Gly Ile Glu	
215 220 225	
cta gaa gat ggc aca gta att cct gcc caa cta gtc att gtg ggc atc	835
Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu Val Ile Val Gly Ile	
230 235 240 245	
ggt gtc att ccg aac aca gaa ctt gcc gct gtt ctg ggc tta gac atc	883
Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val Leu Gly Leu Asp Ile	
250 255 260	
aac aac ggc atc gtg gtg gat aaa cat gcc gtc gcg tca gat ggc acc	931
Asn Asn Gly Ile Val Val Asp Lys His Ala Val Ala Ser Asp Gly Thr	
265 270 275	
acc att gcg att ggc gat gtc gcc aac att ccc aat cca atc cct ggt	979
Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro Asn Pro Ile Pro Gly	
280 285 290	
tcc ccc gct gat gaa cgc atc cga cta gaa agc gtc aat aac gcc atc	1027
Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser Val Asn Asn Ala Ile	
295 300 305	
gag cac gca aag atc gct gca tac tca ctc gtc ggc cag ccc gaa gcc	1075
Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val Gly Gln Pro Glu Ala	
310 315 320 325	

tac gcc gga atc ccc tgg ttc tgg tcc aac caa ggc gat ctc aaa cta 1123  
 Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln Gly Asp Leu Lys Leu  
                   330                                  335                                  340

caa att gca gga ctt acc ctt ggt tat gac agc aca gta atc cga cag 1171  
 Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser Thr Val Ile Arg Gln  
                   345                                  350                                  355

gat ccc gag aaa aag aag ttc tct gtc ctt tat tac cgt ggc gac aac 1219  
 Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr Tyr Arg Gly Asp Asn  
                   360                                  365                                  370

atc atc gcc gcc gat tgt gtc aac gct cca ctg gat ttc atg gct gtg 1267  
 Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu Asp Phe Met Ala Val  
                   375                                  380                                  385

cgc agt gca ctt tcc agg aac caa aat atc ccc gcc gac ctt gct gca 1315  
 Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro Ala Asp Leu Ala Ala  
                   390                                  395                                  400                                  405

gat att tcg cag ccg ctg aaa aaa cta gcc gtt gac ctg gag gtt acc 1363  
 Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val Asp Leu Glu Val Thr  
                   410                                  415                                  420

cga tgactcgcag taatttaccg gct 1389  
 Arg

<210> 678

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

Met Asn Thr Ser Ala Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln  
   1                                  5                                  10                                  15

Ser Gly Val Gln Leu Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu  
                   20                                  25                                  30

Ser Ile Thr Leu Leu Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro  
                   35                                  40                                  45

Ala Leu Ser Lys Glu Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu  
                   50                                  55                                  60

Ile Phe Arg Ser Asn Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val  
                   65                                  70                                  75                                  80

Lys Gly Val Arg Ile Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly  
                   85                                  90                                  95

Val Ala Tyr Gly Ala Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu  
                   100                                  105                                  110

Ala Val Gly Ala Arg Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu  
                   115                                  120                                  125

Glu Gly Val Thr Tyr Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys  
                   130                                  135                                  140

Ala Met Ile Gly Ser Val Thr Asp Ala Val Val Val Gly Gly Gly Phe  
 145 150 155 160  
 Ile Gly Leu Glu Ala Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val  
 165 170 175  
 Thr Val Leu Glu Tyr Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu  
 180 185 190  
 Glu Thr Ala Ala Phe Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn  
 195 200 205  
 Ile Val Leu Asp Ala Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys  
 210 215 220  
 Leu Ser Gly Ile Glu Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu  
 225 230 235 240  
 Val Ile Val Gly Ile Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val  
 245 250 255  
 Leu Gly Leu Asp Ile Asn Asn Gly Ile Val Val Asp Lys His Ala Val  
 260 265 270  
 Ala Ser Asp Gly Thr Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro  
 275 280 285  
 Asn Pro Ile Pro Gly Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser  
 290 295 300  
 Val Asn Asn Ala Ile Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val  
 305 310 315 320  
 Gly Gln Pro Glu Ala Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln  
 325 330 335  
 Gly Asp Leu Lys Leu Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser  
 340 345 350  
 Thr Val Ile Arg Gln Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr  
 355 360 365  
 Tyr Arg Gly Asp Asn Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu  
 370 375 380  
 Asp Phe Met Ala Val Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro  
 385 390 395 400  
 Ala Asp Leu Ala Ala Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val  
 405 410 415  
 Asp Leu Glu Val Thr Arg  
 420

&lt;210&gt; 679

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1051)

&lt;223&gt; RXA00224

&lt;400&gt; 679

gtgatgtcat tgggtgcatcg ggtgctgctg aaaagattgc tgagtacctc gcttcagaga 60

acctcatcta gccactatct tcacaaagga gaacatttaa atg tct att tct tat 115  
 Met Ser Ile Ser Tyr  
 1 5

gtg ctg gtt gag cag cta gat ggc cgc cca gaa cca gtt acc ctt gaa 163  
 Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu Pro Val Thr Leu Glu  
 10 15 20

ttg atc act gct gct cgc gca ctc ggt gac gtc gtt gcc gtt gtc gtt 211  
 Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val Val Ala Val Val Val  
 25 30 35

ggc gag cca ggt gcc ggc gta aac ctt gct gct gag ctc ggc aat tgg 259  
 Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala Glu Leu Gly Asn Trp  
 40 45 50

ggt gca gca cag gtt gtt tcc gct gaa atc tct ggc gct tcc aac cgt 307  
 Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser Gly Ala Ser Asn Arg  
 55 60 65

ttg atc ttg cct gct gtt gat gcg ctg cac att ttg gct gcg aac aac 355  
 Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile Leu Ala Ala Asn Asn  
 70 75 80 85

cca ggt cca att gtt atc gct gca act gca agc ggt aat gag atc gct 403  
 Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser Gly Asn Glu Ile Ala  
 90 95 100

ggt cgt ttg gct gcc cgt ttg gct tct ggt gtg ctc acc gat gtc gtc 451  
 Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val Leu Thr Asp Val Val  
 105 110 115

gga atc aat gcc gac cgc acc gca cag cag tcc att ttc ggc gac acc 499  
 Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser Ile Phe Gly Asp Thr  
 120 125 130

att cag gtg tcc gct gca gtt ggt ggc gct tca ccg ctg tac acc ctg 547  
 Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser Pro Leu Tyr Thr Leu  
 135 140 145

cgt cca ggt gcc ctt gat ggc gtg gcc gtt cct gca acc ggt gaa ttg 595  
 Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro Ala Thr Gly Glu Leu  
 150 155 160 165

gca acc att gag atc cca ggc gca acc gcc aag gat gtc acc atc acc 643  
 Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys Asp Val Thr Ile Thr  
 170 175 180

tcc ttc acg cca agc acc cag agc gat cgc cct gag ctg cca cag gca 691  
 Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro Glu Leu Pro Gln Ala  
 185 190 195

aag gtc gtt atc gca ggt gga cgt ggt gtc gga agc gaa gaa aac ttc 739

Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly Ser Glu Glu Asn Phe  
 200 205 210  
 cgc agc atc gtt gaa cca ctg gca gat gca ttg ggc ggt gcc gtt ggc 787  
 Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu Gly Gly Ala Val Gly  
 215 220 225  
 gca acc cgc gac gcc gtt gat ctg ggc tac tac cca ggc gag tac cag 835  
 Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr Pro Gly Glu Tyr Gln  
 230 235 240 245  
 gtt ggt cag acc ggt gtc acc gtg tcc cca gac ctc tac atc ggc ctc 883  
 Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp Leu Tyr Ile Gly Leu  
 250 255 260  
 ggc att tcc ggt gca att cag cac act tct ggt atg cag acc gca aag 931  
 Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly Met Gln Thr Ala Lys  
 265 270 275  
 aag gtt att gtg atc aac aac gat gag gac gcg ccg atc ttc cag att 979  
 Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala Pro Ile Phe Gln Ile  
 280 285 290  
 gcg gac ctc ggt gtc gtt ggc gac ctc ttt gac atc gcc cct gcg ctc 1027  
 Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp Ile Ala Pro Ala Leu  
 295 300 305  
 atc gaa gag atc aac aag cgc aag taggagtttt gaacactttt tat 1074  
 Ile Glu Glu Ile Asn Lys Arg Lys  
 310 315  
 <210> 680  
 <211> 317  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 680  
 Met Ser Ile Ser Tyr Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu  
 1 5 10 15  
 Pro Val Thr Leu Glu Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val  
 20 25 30  
 Val Ala Val Val Val Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala  
 35 40 45  
 Glu Leu Gly Asn Trp Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser  
 50 55 60  
 Gly Ala Ser Asn Arg Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile  
 65 70 75 80  
 Leu Ala Ala Asn Asn Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser  
 85 90 95  
 Gly Asn Glu Ile Ala Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val  
 100 105 110  
 Leu Thr Asp Val Val Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser  
 115 120 125



Ile Phe Gly Asp Thr Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser  
 130 135 140  
 Pro Leu Tyr Thr Leu Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro  
 145 150 155 160  
 Ala Thr Gly Glu Leu Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys  
 165 170 175  
 Asp Val Thr Ile Thr Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro  
 180 185 190  
 Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly  
 195 200 205  
 Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu  
 210 215 220  
 Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr  
 225 230 235 240  
 Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp  
 245 250 255  
 Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly  
 260 265 270  
 Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala  
 275 280 285  
 Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp  
 290 295 300  
 Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys  
 305 310 315

<210> 681  
 <211> 909  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(886)  
 <223> RXA00225

<400> 681  
 gtaggcgtcg aaaagcaatg ggcgaagccc gcgtagtatg ggcgggcaac gctaaaagcg 60  
 ccaaaaacgc caaaaatcgt gaattgaaag gtgagtgtgg atg tcc aca atc gtg 115  
 Met Ser Thr Ile Val  
 1 5  
 gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa 163  
 Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu  
 10 15 20  
 gct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag 211  
 Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu

25	30	35	
atc aat gag ttt gct ctg gag cag gca ctg cgc ttg cgg gag tcc aac Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn 40 45 50			259
ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly 55 60 65			307
ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala 70 75 80 85			355
atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr 90 95 100			403
gct tgg gcg ctg aac aac gct atc aac acc atc gcg ggt gtt gct ctc Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu 105 110 115			451
atc gtg acg ggt tcg gct tct tcc gat ggt tcc atg ggt gcg ctt cct Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro 120 125 130			499
ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser 135 140 145			547
gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn 150 155 160 165			595
cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tcg att His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile 170 175 180			643
tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met 185 190 195			691
gct gct aag aag gct gag atc aag aag ctt tcc ttg gct gaa atc ggc Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly 200 205 210			739
gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr 215 220 225			787
gct gca gct gat cgt cct gag cgc tcc caa ggt gat gtc att ggt gca Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala 230 235 240 245			835
tcg ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu 250 255 260			883
atc tagccactat cttcacaag gag Ile			909

&lt;210&gt; 682

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 682

Met Ser Thr Ile Val Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser  
 1 5 10 15

Lys Arg Thr Leu Glu Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp  
 20 25 30

Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg  
 35 40 45

Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser  
 50 55 60

Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met  
 65 70 75 80

Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser  
 85 90 95

Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile  
 100 105 110

Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser  
 115 120 125

Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala  
 130 135 140

Leu Thr Asn Leu Ser Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala  
 145 150 155 160

Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro  
 165 170 175

Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn  
 180 185 190

Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser  
 195 200 205

Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala  
 210 215 220

Ala Thr Ala Val Thr Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly  
 225 230 235 240

Asp Val Ile Gly Ala Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu  
 245 250 255

Ala Ser Glu Asn Leu Ile  
 260

&lt;210&gt; 683

966

Ser	Lys	Glu	Gly	Met	Ile	Thr	Ala	Phe	Met	Asp	Ala	Pro	Ile	Gly	Asn		
			190					195					200				
tcc	tat	gtt	gta	tta	ctg	ctg	gtc	ggc	gca	gca	atc	ggc	gcg	gtc	cta	735	
Ser	Tyr	Val	Val	Leu	Leu	Leu	Val	Gly	Ala	Ala	Ile	Gly	Ala	Val	Leu		
		205					210					215					
acc	ttc	aca	tac	tcc	gcg	aaa	ctc	gtg	ctc	ggc	gca	ttc	gtc	gac	ggc	783	
Thr	Phe	Thr	Tyr	Ser	Ala	Lys	Leu	Val	Leu	Gly	Ala	Phe	Val	Asp	Gly		
	220					225					230						
cca	cgc	gac	atg	tca	cac	gtc	aag	gaa	gcc	ccc	gtc	tcc	ctc	tgg	ctt	831	
Pro	Arg	Asp	Met	Ser	His	Val	Lys	Glu	Ala	Pro	Val	Ser	Leu	Trp	Leu		
235					240				245						250		
ccg	gcc	gcc	ctg	cct	gga	ctt	atg	tct	ctg	cca	cta	gtc	cta	gta	ctt	879	
Pro	Ala	Ala	Leu	Pro	Gly	Leu	Met	Ser	Leu	Pro	Leu	Val	Leu	Val	Leu		
				255					260						265		
tcg	ctt	ttc	gac	gcc	ccc	gtc	tcc	gcc	gca	gcc	acc	tcc	gcc	gcg	ggg	927	
Ser	Leu	Phe	Asp	Ala	Pro	Val	Ser	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Gly		
			270					275					280				
gaa	gcg	gcg	cac	atg	cac	ctg	gca	ttg	tgg	cac	ggc	atc	aac	acc	cca	975	
Glu	Ala	Ala	His	Met	His	Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro		
		285					290					295					
ctg	ttg	att	tcc	ttg	ggt	gtg	ctg	gtg	gcc	gga	atc	ctt	ggt	gtg	ctg	1023	
Leu	Leu	Ile	Ser	Leu	Gly	Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu		
	300					305					310						
ttc	cgc	aaa	gag	ctg	tgg	aaa	atc	gcc	gag	acc	agc	cct	ttc	ccc	atc	1071	
Phe	Arg	Lys	Glu	Leu	Trp	Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile		
315					320				325						330		
gcc	aca	ggc	aac	gac	atc	cta	tcg	atg	ctg	gtt	tac	cga	gcc	aac	ttg	1119	
Ala	Thr	Gly	Asn	Asp	Ile	Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu		
			335						340					345			
ctg	ggt	aaa	ttc	ttc	ggt	cgc	atg	gct	gat	tcg	atg	agc	cca	cgc	agg	1167	
Leu	Gly	Lys	Phe	Phe	Gly	Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg		
			350					355					360				
cac	ttg	gtc	agc	ctc	atc	gtg	ctg	ctc	tgg	gcg	ctg	gct	gct	ttt	gcc	1215	
His	Leu	Val	Ser	Leu	Ile	Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala		
		365					370					375					
acc	att	cac	ccc	tcg	gtt	cag	ctt	gca	cca	aag	caa	ccg	gga	att	gat	1263	
Thr	Ile	His	Pro	Ser	Val	Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp		
	380					385					390						
cgt	tgg	atc	gac	ctc	att	ccg	ctt	gcc	atc	atc	gcg	cta	tct	gtc	ttc	1311	
Arg	Trp	Ile	Asp	Leu	Ile	Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe		
395					400					405					410		
ggc	ctg	ctc	acc	acc	cga	aac	cgc	ctc	agc	gca	gcc	gtg	ctt	gtg	ggt	1359	
Gly	Leu	Leu	Thr	Thr	Arg	Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly		
			415					420						425			
acc	gtt	ggt	gtg	ggt	gtt	tcc	ttc	cag	atg	cta	ctt	ctg	ggc	gct	ccc	1407	
Thr	Val	Gly	Val	Gly	Val	Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro		

430	435	440	
gat gtt gca ctt acc cag ttc ctg gta gaa ggc ctc gtc gtg gta atc Asp Val Ala Leu Thr Gln Phe Leu Val Glu Gly Leu Val Val Val Ile 445 450 455			1455
atc atg atg gtt gtc cgg cac cag cct gcc aac ttc aag cgc atc aag Ile Met Met Val Val Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys 460 465 470			1503
ccc agc aga agg cgc agc acc gtt ctt gtc gcc gtc ctt gct gcc ttc Pro Ser Arg Arg Arg Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe 475 480 485 490			1551
gcc gca ttc atg gcg gtg tgg gga ttg ctt ggc cgt cac gaa cgt tct Ala Ala Phe Met Ala Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser 495 500 505			1599
gag ctg gcc atg tgg tac ctc aac caa ggt cca gag atc acc tct ggc Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly 510 515 520			1647
gcc aac gtg gtg aac acc atc ctc gtg gaa ttc cgt gca ctg gat acg Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr 525 530 535			1695
ttg ggc gag ctc tcc gtg ctt ggc atg gca gct gtc gtc atc ggt gcg Leu Gly Glu Leu Ser Val Leu Gly Met Ala Ala Val Val Ile Gly Ala 540 545 550			1743
atg gtg gct tcc atg cct cgt cat ccg ttt gcc aag ggc acc cac cct Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro 555 560 565 570			1791
cgc ccc ttt ggc caa tca cag ttg aac tcc att ccg ctg cgc atg ctg Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu 575 580 585			1839
ctt aag gtg ctg gtt cca gcg cta tgc ttc ttg agc ttc atg gtg ttc Leu Lys Val Leu Val Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe 590 595 600			1887
atg cgt gga cac aat gat ccg gga ggc ggt ttc atc gca gcc cta att Met Arg Gly His Asn Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile 605 610 615			1935
gcc ggt ggc gcg ctg atg ctc ctg tac ctg tcc aag gcc aaa gat ggc Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly 620 625 630			1983
cgc att ttc cgc ccg aat gtt cct ttc att ctc act ggt gcg ggc atc Arg Ile Phe Arg Pro Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile 635 640 645 650			2031
ttg atg gca gtg ttc tcg ggc gta ctg gga ctc acc cac ggt tct ttc Leu Met Ala Val Phe Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe 655 660 665			2079
ctg tac gcc atc cac ttc aac ttc gta ggc cag cac tgg acc acc tcg Leu Tyr Ala Ile His Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser 670 675 680			2127

atg atc ttc gac ctc ggc gtg tac ctg gcc gtg ttg ggc atg gtg tcc 2175  
Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser  
685 690 695

atg gca atc aac ggc ctg ggc gga tac ctg cgc cca ggt acc gac aat 2223  
Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn  
700 705 710

gca gat ctg gac tac gcc cgc cga agt ggc cca ctg cca gca acg cca 2271  
Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro  
715 720 725 730

acg gtt gaa ccc gaa cca gaa ggc gat gaa gac tgg ccc gaa ccc atc 2319  
Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile  
735 740 745

aac ccc gca ggc gat aac aaa gag gag gca aac cga tgattctcgc 2365  
Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala Asn Arg  
750 755

actgacagtc gcg 2378

<210> 684

<211> 758

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

Val Leu Thr Gly Val Ile Ala Val Leu Ile Ala Met Ser Ala Phe Thr  
1 5 10 15

Lys Ser Ala Gln Phe Pro Phe His Phe Trp Leu Pro Glu Ala Met Ala  
20 25 30

Ala Ala Thr Pro Val Ser Ala Phe Leu His Ala Ala Ala Val Val Lys  
35 40 45

Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser Ile Val Phe His Asp Val  
50 55 60

Ala Val Trp Asn Trp Leu Leu Ile Ile Val Gly Met Gly Thr Ala Ile  
65 70 75 80

Met Ser Ala Tyr Phe Ala Val Gln Lys Thr Asp Leu Lys Lys Leu Thr  
85 90 95

Ala Tyr Ser Thr Val Ser His Leu Gly Trp Ile Val Ala Thr Ile Gly  
100 105 110

Val Gly Thr Pro Phe Ala Leu Gly Ala Ala Ile Val His Thr Leu Ser  
115 120 125

His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp  
130 135 140

His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys  
145 150 155 160

Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met

165										170					175				
Ala	Ser	Val	Pro	Pro	Leu	Leu	Gly	Phe	Val	Val	Ser	Lys	Glu	Gly	Met	Ile			
			180					185							190				
Thr	Ala	Phe	Met	Asp	Ala	Pro	Ile	Gly	Asn	Ser	Tyr	Val	Val	Leu	Leu				
		195					200					205							
Leu	Val	Gly	Ala	Ala	Ile	Gly	Ala	Val	Leu	Thr	Phe	Thr	Tyr	Ser	Ala				
	210					215					220								
Lys	Leu	Val	Leu	Gly	Ala	Phe	Val	Asp	Gly	Pro	Arg	Asp	Met	Ser	His				
225					230					235					240				
Val	Lys	Glu	Ala	Pro	Val	Ser	Leu	Trp	Leu	Pro	Ala	Ala	Leu	Pro	Gly				
				245					250					255					
Leu	Met	Ser	Leu	Pro	Leu	Val	Leu	Val	Leu	Ser	Leu	Phe	Asp	Ala	Pro				
			260					265						270					
Val	Ser	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Gly	Glu	Ala	Ala	His	Met	His				
		275					280					285							
Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro	Leu	Leu	Ile	Ser	Leu	Gly				
	290					295					300								
Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu	Phe	Arg	Lys	Glu	Leu	Trp				
305					310						315				320				
Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile	Ala	Thr	Gly	Asn	Asp	Ile				
				325					330					335					
Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu	Leu	Gly	Lys	Phe	Phe	Gly				
			340					345					350						
Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	His	Leu	Val	Ser	Leu	Ile				
		355					360					365							
Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	Thr	Ile	His	Pro	Ser	Val				
					375						380								
Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	Arg	Trp	Ile	Asp	Leu	Ile				
385					390						395				400				
Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	Gly	Leu	Leu	Thr	Thr	Arg				
				405					410					415					
Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly	Val				
			420					425					430						
Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	Gln				
		435					440					445							
Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	Arg				
	450					455					460								
His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	Ser				
465					470						475				480				
Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	Val				
				485				490						495					



Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr  
 500 505 510  
 Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr  
 515 520 525  
 Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val  
 530 535 540  
 Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro  
 545 550 555 560  
 Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser  
 565 570 575  
 Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro  
 580 585 590  
 Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp  
 595 600 605  
 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met  
 610 615 620  
 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn  
 625 630 635 640  
 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser  
 645 650 655  
 Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe  
 660 665 670  
 Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly  
 675 680 685  
 Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu  
 690 695 700  
 Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala  
 705 710 715 720  
 Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro  
 725 730 735  
 Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn  
 740 745 750  
 Lys Glu Glu Ala Asn Arg  
 755

&lt;210&gt; 685

&lt;211&gt; 1872

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1849)

&lt;223&gt; FRXA00606

&lt;400&gt; 685

atggataacc agactggcac gcgcgatatt cgtcgcctcg gtttcctggg caagaaaaat 60

gccgttcacg tttgtgtctg tattaatagg tgcgttgctcg atg gca tcg gtt ccg 115  
Met Ala Ser Val Pro  
1 5

ccg ttg ctc ggc ttc gtg tcc aaa gaa ggc atg atc aca gcg ttc atg 163  
Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile Thr Ala Phe Met  
10 15 20

gac gcc ccc atc ggc aac tcc tat gtt gta tta ctg ctg gtc ggc gca 211  
Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Leu Val Gly Ala  
25 30 35

gca atc ggc gcg gtc cta acc ttc aca tac tcc gcg aaa ctc gtg ctc 259  
Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu  
40 45 50

ggc gca ttc gtc gac ggc cca cgc gac atg tca cac gtc aag gaa gcc 307  
Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His Val Lys Glu Ala  
55 60 65

ccc gtc tcc ctc tgg ctt ccg gcc gcc ctg cct gga ctt atg tct ctg 355  
Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu  
70 75 80 85

cca cta gtc cta gta ctt tcg ctt ttc gac gcc ccc gtc tcc gcc gca 403  
Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro Val Ser Ala Ala  
90 95 100

gcc acc tcc gcc gcg ggg gaa gcg gcg cac atg cac ctg gca ttg tgg 451  
Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp  
105 110 115

cac ggc atc aac acc cca ctg ttg att tcc ttg ggt gtg ctg gtg gcc 499  
His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala  
120 125 130

gga atc ctt ggt gtg ctg ttc cgc aaa gag ctg tgg aaa atc gcc gag 547  
Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu  
135 140 145

acc agc cct ttc ccc atc gcc aca ggc aac gac atc cta tcg atg ctg 595  
Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu  
150 155 160 165

gtt tac cga gcc aac ttg ctg ggt aaa ttc ttc ggt cgc atg gct gat 643  
Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly Arg Met Ala Asp  
170 175 180

tcg atg agc cca cgc agg cac ttg gtc agc ctc atc gtg ctg ctc tgg 691  
Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Leu Trp  
185 190 195

gcg ctg gct gct ttt gcc acc att cac ccc tcg gtt cag ctt gca cca 739  
Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val Gln Leu Ala Pro  
200 205 210

aag caa ccg gga att gat cgt tgg atc gac ctc att ccg ctt gcc atc Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile 215 220 225	787
atc gcg cta tct gtc ttc ggc ctg ctc acc acc cga aac cgc ctc agc Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser 230 235 240 245	835
gca gcc gtg ctt gtg ggt acc gtt ggt gtg ggt gtt tcc ttc cag atg Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met 250 255 260	883
cta ctt ctg ggc gct ccc gat gtt gca ctt acc cag ttc ctg gta gaa Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln Phe Leu Val Glu 265 270 275	931
ggc ctc gtc gtg gta atc atc atg atg gtt gtc cgg cac cag cct gcc Gly Leu Val Val Val Ile Ile Met Met Val Val Arg His Gln Pro Ala 280 285 290	979
aac ttc aag cgc atc aag ccc agc aga agg cgc agc acc gtt ctt gtc Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser Thr Val Leu Val 295 300 305	1027
gcc gtc ctt gct gcc ttc gcc gca ttc atg gcg gtg tgg gga ttg ctt Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val Trp Gly Leu Leu 310 315 320 325	1075
ggc cgt cac gaa cgt tct gag ctg gcc atg tgg tac ctc aac caa ggt Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly 330 335 340	1123
cca gag atc acc tct ggc gcc aac gtg gtg aac acc atc ctc gtg gaa Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr Ile Leu Val Glu 345 350 355	1171
ttc cgt gca ctg gat acg ttg ggc gag ctc tcc gtg ctt ggc atg gca Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val Leu Gly Met Ala 360 365 370	1219
gct gtc gtc atc ggt gcg atg gtg gct tcc atg cct cgt cat ccg ttt Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro Arg His Pro Phe 375 380 385	1267
gcc aag ggc acc cac cct cgc ccc ttt ggc caa tca cag ttg aac tcc Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser 390 395 400 405	1315
att ccg ctg cgc atg ctg ctt aag gtg ctg gtt cca gcg cta tgc ttc Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro Ala Leu Cys Phe 410 415 420	1363
ttg agc ttc atg gtg ttc atg cgt gga cac aat gat ccg gga ggc ggt Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp Pro Gly Gly Gly 425 430 435	1411
ttc atc gca gcc cta att gcc ggt ggc gcg ctg atg ctc ctg tac ctg Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu 440 445 450	1459
tcc aag gcc aaa gat ggc cgc att ttc cgc ccg aat gtt cct ttc att	1507

Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn Val Pro Phe Ile  
 455 460 465

ctc act ggt gcg ggc atc ttg atg gca gtg ttc tcg ggc gta ctg gga 1555  
 Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser Gly Val Leu Gly  
 470 475 480 485

ctc acc cac ggt tct ttc ctg tac gcc atc cac ttc aac ttc gta ggc 1603  
 Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe Asn Phe Val Gly  
 490 495 500

cag cac tgg acc acc tcg atg atc ttc gac ctc ggc gtg tac ctg gcc 1651  
 Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly Val Tyr Leu Ala  
 505 510 515

gtg ttg ggc atg gtg tcc atg gca atc aac ggc ctg ggc gga tac ctg 1699  
 Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu  
 520 525 530

cgc cca ggt acc gac aat gca gat ctg gac tac gcc cgc cga agt ggc 1747  
 Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly  
 535 540 545

cca ctg cca gca acg cca acg gtt gaa ccc gaa cca gaa ggc gat gaa 1795  
 Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro Glu Gly Asp Glu  
 550 555 560 565

gac tgg ccc gaa ccc atc aac ccc gca ggc gat aac aaa gag gag gca 1843  
 Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala  
 570 575 580

aac cga tgattctcgc actgacagtc gcg 1872  
 Asn Arg

<210> 686  
 <211> 583  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 686  
 Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met  
 1 5 10 15  
 Ile Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu  
 20 25 30  
 Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser  
 35 40 45  
 Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser  
 50 55 60  
 His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro  
 65 70 75 80  
 Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala  
 85 90 95  
 Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met

100					105					110						
His	Leu	Ala	Leu	Trp	His	Gly	Ile	Asn	Thr	Pro	Leu	Leu	Ile	Ser	Leu	
115					120					125						
Gly	Val	Leu	Val	Ala	Gly	Ile	Leu	Gly	Val	Leu	Phe	Arg	Lys	Glu	Leu	
130					135					140						
Trp	Lys	Ile	Ala	Glu	Thr	Ser	Pro	Phe	Pro	Ile	Ala	Thr	Gly	Asn	Asp	
145					150					155					160	
Ile	Leu	Ser	Met	Leu	Val	Tyr	Arg	Ala	Asn	Leu	Leu	Gly	Lys	Phe	Phe	
165					170					175						
Gly	Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	His	Leu	Val	Ser	Leu	
180					185					190						
Ile	Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	Thr	Ile	His	Pro	Ser	
195					200					205						
Val	Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	Arg	Trp	Ile	Asp	Leu	
210					215					220						
Ile	Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	Gly	Leu	Leu	Thr	Thr	
225					230					235					240	
Arg	Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly	
245					250					255						
Val	Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	
260					265					270						
Gln	Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	
275					280					285						
Arg	His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	
290					295					300						
Ser	Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	
305					310					315					320	
Val	Trp	Gly	Leu	Leu	Gly	Arg	His	Glu	Arg	Ser	Glu	Leu	Ala	Met	Trp	
325					330					335						
Tyr	Leu	Asn	Gln	Gly	Pro	Glu	Ile	Thr	Ser	Gly	Ala	Asn	Val	Val	Asn	
340					345					350						
Thr	Ile	Leu	Val	Glu	Phe	Arg	Ala	Leu	Asp	Thr	Leu	Gly	Glu	Leu	Ser	
355					360					365						
Val	Leu	Gly	Met	Ala	Ala	Val	Val	Ile	Gly	Ala	Met	Val	Ala	Ser	Met	
370					375					380						
Pro	Arg	His	Pro	Phe	Ala	Lys	Gly	Thr	His	Pro	Arg	Pro	Phe	Gly	Gln	
385					390					395					400	
Ser	Gln	Leu	Asn	Ser	Ile	Pro	Leu	Arg	Met	Leu	Leu	Lys	Val	Leu	Val	
405					410					415						
Pro	Ala	Leu	Cys	Phe	Leu	Ser	Phe	Met	Val	Phe	Met	Arg	Gly	His	Asn	
420					425					430						

Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu  
 435 440 445  
 Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro  
 450 455 460  
 Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe  
 465 470 475 480  
 Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His  
 485 490 495  
 Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu  
 500 505 510  
 Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly  
 515 520 525  
 Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr  
 530 535 540  
 Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu  
 545 550 555 560  
 Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp  
 565 570 575  
 Asn Lys Glu Glu Ala Asn Arg  
 580

<210> 687  
 <211> 1653  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1630)  
 <223> RXN00595

<400> 687  
 cgacgacacc cgggtccatcg aaccagatga cgatcaatcg cctttgacta ctacgcgctcg 60  
 ttcagtcacc aaccacaacag atcaggagga taaagcttaa atg gcc atg gat gtt 115  
 Met Ala Met Asp Val  
 1 5  
 ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg 163  
 Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala  
 10 15 20  
 gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211  
 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val  
 25 30 35  
 cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct 259  
 Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala  
 40 45 50

gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val 55 60 65	307
gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr 70 75 80 85	355
acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly 90 95 100	403
gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr 105 110 115	451
ggc gtc aac ggt gct ctg ctg act gcc gat ctg ttc aac ttc ttt gtg Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val 120 125 130	499
ttc atc gaa gtg atg ctg ctg cct tcc tat ggt ttg atc gcc atg acc Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr 135 140 145	547
gga acg tgg gcg cgc cta gcc tct gga cga atc ttc gta cta gtc aat Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn 150 155 160 165	595
ctc tct gcc tcc aca ttg ctg gtt gca ggt gtg gga atc gtc tac ggt Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly 170 175 180	643
gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly 185 190 195	691
aac ccc ctg gtt gcc agc gca atg ggc atc gtg gtt att gcc atc gcg Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala 200 205 210	739
gtt aaa gcc ggt gta ttc cca gtg cac aca tgg ctg cca cgc acc tat Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr 215 220 225	787
cct ggt aca tca gca gct gtg atg ggg ttg ttc tcc ggt ttg cac acc Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr 230 235 240 245	835
aaa gtc gcg gta tac atg ctc tat cgc att tgg gtc cac att ttt aac Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp Val His Ile Phe Asn 250 255 260	883
atg gat ccc acg tgg aat tgg ctg att gtc gca ttc atg gtg ata tcc Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala Phe Met Val Ile Ser 265 270 275	931
atg ctg gtc ggt ggc ttc gct gga ctt gct gaa aac tcc atc cgt cgc Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu Asn Ser Ile Arg Arg 280 285 290	979
gtc ctt gcc tac caa atg gtc aac ggc atg cca ttt att ctc atc atg	1027

Val	Leu	Ala	Tyr	Gln	Met	Val	Asn	Gly	Met	Pro	Phe	Ile	Leu	Ile	Met		
295						300					305						
atg	gcg	ttt	acc	tct	gac	gat	cca	cag	cgc	gca	ctt	gcc	gct	ggt	ctg	1075	
Met	Ala	Phe	Thr	Ser	Asp	Asp	Pro	Gln	Arg	Ala	Leu	Ala	Ala	Gly	Leu		
310					315					320					325		
ttg	tac	acc	ctg	cac	cac	atg	atc	acc	atc	gcc	gca	ttg	gtg	ctc	act	1123	
Leu	Tyr	Thr	Leu	His	His	Met	Ile	Thr	Ile	Ala	Ala	Leu	Val	Leu	Thr		
				330						335				340			
tcc	ggc	gca	atc	gaa	gaa	acc	tac	ggc	acc	ggt	atg	ttg	tcc	aag	ctg	1171	
Ser	Gly	Ala	Ile	Glu	Glu	Thr	Tyr	Gly	Thr	Gly	Met	Leu	Ser	Lys	Leu		
			345					350					355				
tct	ggc	ctt	gca	cgc	cgc	gaa	ccc	gtc	gtc	gca	gca	gtg	ttc	gct	gca	1219	
Ser	Gly	Leu	Ala	Arg	Arg	Glu	Pro	Val	Val	Ala	Ala	Val	Phe	Ala	Ala		
		360					365					370					
ggt	gcc	ttc	tct	gtt	gtc	ggt	ttc	cca	ccg	ttt	tcc	ggt	atg	tgg	ggc	1267	
Gly	Ala	Phe	Ser	Val	Val	Gly	Phe	Pro	Pro	Phe	Ser	Gly	Met	Trp	Gly		
		375				380					385						
aaa	gcg	ctc	atc	ctg	ctc	gag	atc	gcc	cgc	gtc	ggc	aat	att	gca	gca	1315	
Lys	Ala	Leu	Ile	Leu	Leu	Glu	Ile	Ala	Arg	Val	Gly	Asn	Ile	Ala	Ala		
390					395					400				405			
tgg	atc	gca	atc	gcc	gcc	atc	atc	atc	gcc	agc	ctg	ggc	gca	ctg	ctc	1363	
Trp	Ile	Ala	Ile	Ala	Ala	Ile	Ile	Ile	Ala	Ser	Leu	Gly	Ala	Leu	Leu		
				410					415					420			
tcg	atg	atc	cgc	gtg	tgg	cgt	gaa	gtc	ttc	tgg	ggt	ggc	gca	atg	cac	1411	
Ser	Met	Ile	Arg	Val	Trp	Arg	Glu	Val	Phe	Trp	Gly	Gly	Ala	Met	His		
			425					430					435				
cag	cgc	ggc	gtc	tcg	ccg	cag	ctg	cgc	atc	agc	cca	gca	aaa	atc	gcc	1459	
Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser	Pro	Ala	Lys	Ile	Ala		
		440					445					450					
cca	gcg	ctc	agc	ctg	atc	att	tta	tcg	gta	ggc	atg	ttc	atc	ttc	gcg	1507	
Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly	Met	Phe	Ile	Phe	Ala		
		455				460					465						
ggc	ccg	ctt	atc	gac	gcg	acc	ctc	acc	gcc	acc	gac	ggc	ctc	ttg	aac	1555	
Gly	Pro	Leu	Ile	Asp	Ala	Thr	Leu	Thr	Ala	Thr	Asp	Gly	Leu	Leu	Asn		
470					475					480				485			
acc	gat	gca	tac	caa	cag	gct	gtg	ctc	ggt	gaa	aat	gcc	atc	gga	gtg	1603	
Thr	Asp	Ala	Tyr	Gln	Gln	Ala	Val	Leu	Gly	Glu	Asn	Ala	Ile	Gly	Val		
				490					495					500			
cca	agc	cct	agc	tac	cag	gga	gga	aac	taatgcttaa	cgccctgaaa						1650	
Pro	Ser	Pro	Ser	Tyr	Gln	Gly	Gly	Asn									
			505				510										
ttc																1653	

<210> 688  
 <211> 510  
 <212> PRT



<213> *Corynebacterium glutamicum*

&lt;400&gt; 688

```

Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala
 1           5           10           15

Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile
      20           25           30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
      35           40           45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
      50           55           60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
      65           70           75           80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
      85           90           95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
      100          105          110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
      115          120          125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
      130          135          140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
      145          150          155          160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
      165          170          175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
      180          185          190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
      195          200          205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
      210          215          220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
      225          230          235          240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp
      245          250          255

Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala
      260          265          270

Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu
      275          280          285

Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro
      290          295          300

Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala

```

980

Val	Leu	Leu	Pro	Trp	Arg	Leu	Ile	Arg	Asp	Ile	Leu	His	Ile	Ile	Val		
			25					30					35				
cct	ttc	gcg	ggg	att	ttt	gct	ggc	atc	ttg	ttg	ttt	gca	cac	acc	gct	259	
Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu	Phe	Ala	His	Thr	Ala		
		40					45					50					
gaa	cac	ggc	ccg	att	gct	cac	aac	gtg	ggc	ctt	tat	gtc	ggg	ggc	gtg	307	
Glu	His	Gly	Pro	Ile	Ala	His	Asn	Val	Gly	Leu	Tyr	Val	Gly	Gly	Val		
	55					60					65						
gca	atc	ccc	ttt	gct	gcc	gat	acg	ttc	agc	gcc	atc	atg	ttg	atc	acc	355	
Ala	Ile	Pro	Phe	Ala	Ala	Asp	Thr	Phe	Ser	Ala	Ile	Met	Leu	Ile	Thr		
	70				75				80						85		
acc	tcg	atc	gtt	gcg	gtg	gct	gcc	aac	ttg	ttt	gcc	acc	atc	gtc	ggg	403	
Thr	Ser	Ile	Val	Ala	Val	Ala	Ala	Asn	Trp	Phe	Ala	Thr	Ile	Val	Gly		
				90				95						100			
gaa	acc	cgc	gcg	cgt	ttc	tat	cca	gcg	ctc	aca	ttg	atg	ctg	atc	acg	451	
Glu	Thr	Arg	Ala	Arg	Phe	Tyr	Pro	Ala	Leu	Thr	Leu	Met	Leu	Ile	Thr		
			105					110					115				
ggc	gtc	aac	ggg	gct	ctg	ctg	act	gcc	gat	ctg	ttc	aac	ttc	ttt	gtg	499	
Gly	Val	Asn	Gly	Ala	Leu	Leu	Thr	Ala	Asp	Leu	Phe	Asn	Phe	Phe	Val		
		120					125					130					
ttc	atc	gaa	gtg	atg	ctg	ctg	cct	tcc	tat	ggg	ttg	atc	gcc	atg	acc	547	
Phe	Ile	Glu	Val	Met	Leu	Leu	Pro	Ser	Tyr	Gly	Leu	Ile	Ala	Met	Thr		
	135					140					145						
gga	acg	tgg	gcg	cgc	cta	gcc	tct	gga	cga	atc	ttc	gta	cta	gtc	aat	595	
Gly	Thr	Trp	Ala	Arg	Leu	Ala	Ser	Gly	Arg	Ile	Phe	Val	Leu	Val	Asn		
	150				155				160						165		
ctc	tct	gcc	tcc	aca	ttg	ctg	gtt	gca	ggg	gtg	gga	atc	gtc	tac	ggg	643	
Leu	Ser	Ala	Ser	Thr	Leu	Leu	Val	Ala	Gly	Val	Gly	Ile	Val	Tyr	Gly		
				170					175					180			
gtc	ata	ggc	tca	gtc	aac	atc	gca	gct	ctg	caa	gat	gtc	gta	gag	ggc	691	
Val	Ile	Gly	Ser	Val	Asn	Ile	Ala	Ala	Leu	Gln	Asp	Val	Val	Glu	Gly		
			185				190						195				
aac	ccc	ctg	gtt	gcc	agc	gca	atg	ggc	atc	gtg	gtt	att	gcc	atc	gcg	739	
Asn	Pro	Leu	Val	Ala	Ser	Ala	Met	Gly	Ile	Val	Val	Ile	Ala	Ile	Ala		
		200					205					210					
gtt	aaa	gcc	ggg	gta	ttc	cca	gtg	cac	aca	tgg	ctg	cca	cgc	acc	tat	787	
Val	Lys	Ala	Gly	Val	Phe	Pro	Val	His	Thr	Trp	Leu	Pro	Arg	Thr	Tyr		
	215					220					225						
cct	ggg	aca	tca	gca	gct	gtg	atg	ggg	ttg	ttc	tcc	ggg	ttg	cac	acc	835	
Pro	Gly	Thr	Ser	Ala	Ala	Val	Met	Gly	Leu	Phe	Ser	Gly	Leu	His	Thr		
	230				235				240						245		
aaa	gtc	gcg	gta	tac	atg	ctc	tat	cgc	att							865	
Lys	Val	Ala	Val	Tyr	Met	Leu	Tyr	Arg	Ile								
			250					255									

&lt;210&gt; 690

<211> 255  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 690

```

Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala
 1           5           10           15

Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile
          20           25           30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
 35           40           45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
 50           55           60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
 65           70           75           80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
          85           90           95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
          100          105          110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
 115          120          125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
 130          135          140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
 145          150          155          160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
          165          170          175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
          180          185          190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
          195          200          205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
 210          215          220

Leu Pro Arg Thr' Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
 225          230          235          240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile
          245          250          255

```

<210> 691  
 <211> 2118  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS

&lt;222&gt; (1)..(2118)

&lt;223&gt; RXA00913

&lt;400&gt; 691

att att tcc gtg gtg ggc att ggt acc cgc gaa gct ttg ctg gca ggt	48
Ile Ile Ser Val Val Gly Ile Gly Thr Arg Glu Ala Leu Leu Ala Gly	
1 5 10 15	
ctt gca ctg acc gtt gcg cac tcc ttg ttt aag gca aca ttg ttc atg	96
Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met	
20 25 30	
aca gtt ggt gcc att gac cac acc acc gga act cgt gat att cgt aaa	144
Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys	
35 40 45	
ctc tcc ggt ctg tgg cgt aaa caa ccg atc ctg ttc gcc gtt gct gct	192
Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala	
50 55 60	
gtt tcg gcg gcg tcc atg gct ggt att ccg cca ctg ttt ggt ttt atc	240
Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile	
65 70 75 80	
gcc aag gaa aca gcg ctg gat acc gtg ttg aat gag cag atg ttg cat	288
Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His	
85 90 95	
ggc atg cca ggt cga ttg atg ctg gct ggc atc gtt ttg ggt tcc atc	336
Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile	
100 105 110	
ttc acc atg gca tat tcc tgc tac ttc ctg tac gaa gcc ttt gcc acg	384
Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr	
115 120 125	
aag cac tcc aaa ttc cca gag gcc aac ggt gtc tca cct gca gtg gag	432
Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu	
130 135 140	
gca atg cat ccg gtg aag ttt aag ctg tgg atc gca cct gtc atc ctg	480
Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu	
145 150 155 160	
gct att ttg acc gta gtg ttt ggt gtt ttc ccc aag cca gtg tcg gaa	528
Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu	
165 170 175	
gca att gtc acg cat ctt gat aac gtc acg cca tcg ctt gat gat gtc	576
Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val	
180 185 190	
cac acc aaa ctg gcc ttg tgg cat ggt ctg aat cta ccg ctg ctg ctg	624
His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu	
195 200 205	
tct gtg gtg atc atc att tcc gga ttc atc atc ttc tgg gag cga gac	672
Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp	
210 215 220	
acc gtc gaa cgt ttg cgc cct aac acc gca gcg ttt ggc agt gcc gat	720

Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp	
225 230 235 240	
acc gcc tac gac gcc att ctt gat gca ctg cgt gtg ctc tcc cac cgc	768
Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg	
245 250 255	
ctg act gca tcc acc cag cgt ggt tct ttg acc ctg aac gtc ggt gtg	816
Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val	
260 265 270	
atc ttc ttc gtc ctc acg att gtt ccg ctg atc gct ttg atc act ggc	864
Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly	
275 280 285	
gaa caa agc gat gtc cgc atg gag ctg tgg gat agc cct att cag ggc	912
Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly	
290 295 300	
ttc atc gcg gcc atc att atc gtc gtt gcg att gtg gca acc acc atg	960
Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met	
305 310 315 320	
gat aac cgt ttg tct gcg ctg att ttg gtg ggt gtg aca ggt tat ggc	1008
Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly	
325 330 335	
att gcc gtt atc ttc gcg cta cat ggc gca ccg gac ttg gcg cta acc	1056
Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr	
340 345 350	
cag gtg ctg gtg gag acc atc gtc atg gtg gta ttc atg ctg gtg ctg	1104
Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu	
355 360 365	
cgt aaa atg ccg aca gaa gtt gcg tgg aag gca gaa cct aaa cag tct	1152
Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser	
370 375 380	
cgc gtg cga gcg tgg ctt gct ggc gcc acc gga ttg tcc gtt gtt att	1200
Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile	
385 390 395 400	
gtc acc att ttt gcc atg aat gct cgc acc act gaa ccg atc tct gta	1248
Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val	
405 410 415	
tac atg cag gat ctg gcc tat gag atc gga cat ggc gca aac acc gtc	1296
Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val	
420 425 430	
aac gta ctg ctc gta gac ctg cgt ggt ttt gat acc ttc ggt gaa att	1344
Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile	
435 440 445	
tcc gtc ctt gtg atc gcg gca acc ggt atc gcc tcc ctg gtc tac cga	1392
Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg	
450 455 460	
aac cgc agc ttc cgc aag gat tct cgc aga cca acc ctg gct acc act	1440
Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr	

465	470	475	480	
ggt cgc cgt tgg	ttg gct gct gct gtt	gat acc gaa agg gcg	cag aac	1488
Gly Arg Arg Trp	Leu Ala Ala Ala Val	Asp Thr Glu Arg Ala	Gln Asn	
	485	490	495	
cgc tcg ctg atg	gtt gat gtg gca acg	cgc atc ctc ttc	cct gcc atg	1536
Arg Ser Leu Met	Val Asp Val Ala Thr	Arg Ile Leu Phe	Pro Ala Met	
	500	505	510	
atc atg ttg tct	gtg tac ttc ttc ttc	gcc gga cac aac	gcg ccg ggc	1584
Ile Met Leu Ser	Val Tyr Phe Phe Phe	Ala Gly His Asn	Ala Pro Gly	
	515	520	525	
ggc gga ttc gcc	ggc ggc ctt gtt	gcc tcc ttg gcg	ttc gcc ttg cgc	1632
Gly Gly Phe Ala	Gly Gly Leu Val	Ala Ser Leu Ala	Phe Ala Leu Arg	
	530	535	540	
tac ctt gcc ggt	gga cgt gaa gaa	ctt gaa gaa gcg	ttg cct atc gac	1680
Tyr Leu Ala Gly	Gly Arg Glu Glu	Leu Glu Glu Ala	Leu Pro Ile Asp	
	545	550	555	560
gcc ggc cgt atc	ttg gga act gga	cta ttt gtt tct	gca act gca gtg	1728
Ala Gly Arg Ile	Leu Gly Thr Gly	Leu Phe Val Ser	Ala Thr Ala Val	
	565	570	575	
ctg tgg ccc atg	gtt ctt ctt ggt	gaa cca ccg ctg	acc tcc cat att	1776
Leu Trp Pro Met	Val Leu Leu Gly	Glu Pro Pro Leu	Thr Ser His Ile	
	580	585	590	
tgg gat ctc aca	ctg cca ctt atc	ggt gag att cac	att gca tcc gcg	1824
Trp Asp Leu Thr	Leu Pro Leu Ile	Gly Glu Ile His	Ile Ala Ser Ala	
	595	600	605	
ctg ctc ttt gac	ctt ggt gtc tac	ctg atc gtc atc	ggt ttg acc atg	1872
Leu Leu Phe Asp	Leu Gly Val Tyr	Leu Ile Val Ile	Gly Leu Thr Met	
	610	615	620	
cac att ctc aac	agt ttg ggc ggc	cag ctc gac cg	gat gag gaa atg	1920
His Ile Leu Asn	Ser Leu Gly Gly	Gln Leu Asp Arg	Asp Glu Glu Met	
	625	630	635	640
cgt aag cag cgt	gcg cgc gac cga	gct cga cg	ttg gcg cg	1968
Arg Lys Gln Arg	Ala Arg Asp Arg	Ala Arg Arg Leu	Ala Arg Asn Gln	
	645	650	655	
cgt cga gaa gca	gca acc gtc ggc	gca cg	agg tcg aac	2016
Arg Arg Glu Ala	Ala Thr Val Gly	Ala Arg Arg Ser	Asn Glu Lys Ser	
	660	665	670	
aca cgc caa atg	ccg acg att cg	ggt cct cca ggg	gca gac aca gaa	2064
Thr Arg Gln Met	Pro Thr Ile Arg	Pro Pro Gly Ala	Asp Thr Glu Ser	
	675	680	685	
gtg gag cag aac	ggt gag aac cag	acg tcg ata ag	aca aag cgt tta	2112
Val Glu Gln Asn	Gly Glu Asn Gln	Thr Ser Ile Ser	Thr Lys Arg Leu	
	690	695	700	
aag cag				2118
Lys Gln				
705				

<210> 692  
 <211> 706  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 692  
 Ile Ile Ser Val Val Gly Ile Gly Thr Arg Glu Ala Leu Leu Ala Gly  
 1 5 10 15  
 Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met  
 20 25 30  
 Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys  
 35 40 45  
 Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala  
 50 55 60  
 Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile  
 65 70 75 80  
 Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His  
 85 90 95  
 Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile  
 100 105 110  
 Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr  
 115 120 125  
 Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu  
 130 135 140  
 Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu  
 145 150 155 160  
 Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu  
 165 170 175  
 Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val  
 180 185 190  
 His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu  
 195 200 205  
 Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp  
 210 215 220  
 Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp  
 225 230 235 240  
 Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg  
 245 250 255  
 Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val  
 260 265 270  
 Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly  
 275 280 285



Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly  
 290 295 300  
 Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met  
 305 310 315 320  
 Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly  
 325 330 335  
 Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr  
 340 345 350  
 Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu  
 355 360 365  
 Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser  
 370 375 380  
 Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile  
 385 390 395 400  
 Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val  
 405 410 415  
 Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val  
 420 425 430  
 Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile  
 435 440 445  
 Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg  
 450 455 460  
 Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr  
 465 470 475 480  
 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn  
 485 490 495  
 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met  
 500 505 510  
 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly  
 515 520 525  
 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg  
 530 535 540  
 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp  
 545 550 555 560  
 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val  
 565 570 575  
 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile  
 580 585 590  
 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala  
 595 600 605

Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met  
 610 615 620  
 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met  
 625 630 635 640  
 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln  
 645 650 655  
 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser  
 660 665 670  
 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser  
 675 680 685  
 Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu  
 690 695 700  
 Lys Gln  
 705

<210> 693  
 <211> 955  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(955)  
 <223> RXA00909

<400> 693  
 tcgatgtgtg ttgctaactg ggggtggcac gcacgttggc gttgttgttt ggtgtggctc 60  
 cagagtaatc cacaacgcgc aaaggggaac tggagaacac gtg ctc att ctt ttt 115  
 Val Leu Ile Leu Phe  
 1 5  
 ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act 163  
 Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr  
 10 15 20  
 ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211  
 Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly  
 25 30 35  
 ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga 259  
 Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly  
 40 45 50  
 ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat 307  
 Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn  
 55 60 65  
 atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355  
 Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val  
 70 75 80 85  
 tta ggc gtg ggc gcc cta gtg ctg ctg tac tgc tgg gga tat ttt gat 403  
 Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp

90	95	100	
tcc aac gcg ggt cgc ctc agt gcc ttt ggt gct gaa ctg gtg gcc ttc Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala Glu Leu Val Ala Phe 105 110 115			451
gcc atg gcg atg ttt ggt ctt gtc att tca gac aac atc ctg ctg atg Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met 120 125 130			499
tac gtc ttc tgg gaa atc acc tcc gtt tta tcc ttc ctc ctg gtt ggt Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser Phe Leu Leu Val Gly 135 140 145			547
tat tac ggc gaa cgc gca tct tca cgt cgc tct gca ggt caa gcc ttg Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu 150 155 160 165			595
atg gtg acc acc ctg ggt gga ttg gcc atg ctg gtg ggc atc att ttg Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu 170 175 180			643
atg ggt acc caa act ggc gtg tgg cga ttc tct gag atc cct gcc tac Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr 185 190 195			691
tca agc tcc tgg gca gat gtg ccg tat att tcc gct gct gct gcc ctt Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Ala Leu 200 205 210			739
atc ttg gct ggc gca cta tcc aaa tcg gct atc gca cca acc cac ttc Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile Ala Pro Thr His Phe 215 220 225			787
tgg ctt ccc ggc gcg atg gcc gca cca acg ccg gtg tct gct tac ctg Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu 230 235 240 245			835
cac tcc gca gcg atg gtg aag gcg ggt att tac ctt gtg gct cgc ctc His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu 250 255 260			883
tct cca gac ctc aac gta gtt ggt tcg tgg tac ctg atc atc atc ccg Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Ile Pro 265 270 275			931
ttg ggc atg ttg acc atg ctc atg Leu Gly Met Leu Thr Met Leu Met 280 285			955

&lt;210&gt; 694

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 694

Val	Leu	Ile	Leu	Phe	Leu	Ala	Leu	Thr	Ala	Ala	Ala	Val	Val	Ala	Pro
1				5				10						15	

Ile Leu Ile Arg Thr Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu

20	25	30
Val Pro Gly Ile Gly Phe Phe Trp	Val Leu Ser Glu Phe Ile Lys Gly	
35	40	45
Thr Phe Lys Asp Gly Gly Glu Leu Leu His Tyr Ala Trp Met Pro		
50	55	60
Ser Ala His Leu Asn Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu		
65	70	75
Phe Ser Leu Ile Val Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys		
85	90	95
Trp Gly Tyr Phe Asp Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala		
100	105	110
Glu Leu Val Ala Phe Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp		
115	120	125
Asn Ile Leu Leu Met Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser		
130	135	140
Phe Leu Leu Val Gly Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser		
145	150	155
Ala Gly Gln Ala Leu Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu		
165	170	175
Val Gly Ile Ile Leu Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser		
180	185	190
Glu Ile Pro Ala Tyr Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser		
195	200	205
Ala Ala Ala Ala Leu Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile		
210	215	220
Ala Pro Thr His Phe Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro		
225	230	235
Val Ser Ala Tyr Leu His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr		
245	250	255
Leu Val Ala Arg Leu Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr		
260	265	270
Leu Ile Ile Ile Pro Leu Gly Met Leu Thr Met Leu Met		
275	280	285

&lt;210&gt; 695

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(904)

&lt;223&gt; RXA00700

&lt;400&gt; 695

```

acgccccaca agtcgcaaaa atcaccgccg gcattccaaga ggaatcacac tggctcacag 60

tctcgcccggt gaaagctgcg ctagggcatg gtgaaatctc atg atc aac gcc atc 115
                               Met Ile Asn Ala Ile
                               1           5

aca ctc aag ccc aaa acc ttc ctc acc tta agc ttc ctt gcg gtt ttg 163
Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser Phe Leu Ala Val Leu
                10                15                20

agc atc gtg att ttc ttc tgg ccg ctg atc gtc aac ccg gaa tcc ttc 211
Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val Asn Pro Glu Ser Phe
                25                30                35

ctg tcc gac aaa gcc caa gcg ccc ctc tac atc gcg atc gtc att ccc 259
Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile Ala Ile Val Ile Pro
                40                45                50

ctc gtg ctg gcc gct gtc atc gcc gaa atc agt gaa aac gga ttc gac 307
Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser Glu Asn Gly Phe Asp
                55                60                65

gtt aaa gcc gta gcc atg ctc ggc gtc ctc acc gcc atg gtt gcc gta 355
Val Lys Ala Val Ala Met Leu Gly Val Leu Thr Ala Met Val Ala Val
                70                75                80                85

gtc cga cca ttc ggt gcc ggc gca gca ggc ttt gaa gca gtc ttc ttt 403
Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe Glu Ala Val Phe Phe
                90                95                100

gtc ctc atc ctc ggc gga cga gcc ttc gga ccc ggc ttc gga ttc atc 451
Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro Gly Phe Gly Phe Ile
                105                110                115

ctc ggc aac acc gga ctg ttc gca tcc gcg ctg ctc acc gca gga atc 499
Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu Leu Thr Ala Gly Ile
                120                125                130

gga ccg tgg ctc ccc tac caa atg ctc gca gcc gcc tgg gtc agc ttc 547
Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala Ala Trp Val Ser Phe
                135                140                145

ggc gcc ggc cta ctc ccc caa gta cgc ggc aaa aag gaa atg ctc atc 595
Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys Lys Glu Met Leu Ile
                150                155                160                165

atc gtc cta tac gcc atc gtc tct tca ctc ggc tac gga acc atg atg 643
Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly Tyr Gly Thr Met Met
                170                175                180

aac atg agc ttc tgg ccc tac gcc atc ggt gtc acc agc ggg ctt tcc 691
Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val Thr Ser Gly Leu Ser
                185                190                195

ttc aca ccc ggc gcg ccc gtc ctg gaa aac ctc cac acc ttc atg ctg 739
Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu His Thr Phe Met Leu
                200                205                210

ttc tgc ctc acc aca tcc atg ggt tgg gat ctc ggc cgc gcc ttc ttc 787
Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu Gly Arg Ala Phe Phe

```

215                      220                      225  
 acc tca gtg cta tta ctg ctc aca gcc aaa ccc gtt tta ggt gct tta 835  
 Thr Ser Val Leu Leu Leu Leu Thr Ala Lys Pro Val Leu Gly Ala Leu  
 230                      235                      240                      245  
 cga cgc gcc agc cgc cgc gcc gct ttc ggc gtc gag cgt gac ttc ggg 883  
 Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val Glu Arg Asp Phe Gly  
 250                      255                      260  
 gag gcc ggg gtg cct cgg gtc taaagatttt gttggcttgc ttc 927  
 Glu Ala Gly Val Pro Arg Val  
 265  
 <210> 696  
 <211> 268  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 696  
 Met Ile Asn Ala Ile Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser  
 1                      5                      10                      15  
 Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val  
 20                      25                      30  
 Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile  
 35                      40                      45  
 Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser  
 50                      55                      60  
 Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr  
 65                      70                      75                      80  
 Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe  
 85                      90                      95  
 Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro  
 100                      105                      110  
 Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu  
 115                      120                      125  
 Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala  
 130                      135                      140  
 Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys  
 145                      150                      155                      160  
 Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly  
 165                      170                      175  
 Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val  
 180                      185                      190  
 Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu  
 195                      200                      205  
 His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu



ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att	547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile	
135 140 145	
att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag	595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu	
150 155 160 165	
cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag	643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu	
170 175 180	
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat	691
Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp	
185 190 195	
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg	739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser	
200 205 210	
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg	787
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu	
215 220 225	
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta	835
Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu	
230 235 240 245	
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct	883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser	
250 255 260	
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac	931
Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His	
265 270 275	
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat	979
Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr	
280 285 290	
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt	1027
Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val	
295 300 305	
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc	1075
Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly	
310 315 320 325	
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc	1123
Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val	
330 335 340	
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att	1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile	
345 350 355	
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg	1219
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp	
360 365 370	
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc	1267



Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly  
 375 380 385  
 gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315  
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp  
 390 395 400 405  
 tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363  
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala  
 410 415 420  
 gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411  
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp  
 425 430 435  
 aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459  
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro  
 440 445 450  
 aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507  
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His  
 455 460 465  
 gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555  
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg  
 470 475 480 485  
 aaa ctc act taatcgacaga gtaggcgtct aaa 1587  
 Lys Leu Thr

&lt;210&gt; 698

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 698

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr  
 1 5 10 15  
 Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys  
 20 25 30  
 Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu  
 35 40 45  
 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val  
 50 55 60  
 Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp  
 65 70 75 80  
 Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala  
 85 90 95  
 Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro  
 100 105 110  
 Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu  
 115 120 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu  
 130 135 140  
 Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile  
 145 150 155 160  
 Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile  
 165 170 175  
 Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu  
 180 185 190  
 Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile  
 195 200 205  
 Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala  
 210 215 220  
 Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu  
 225 230 235 240  
 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val  
 245 250 255  
 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala  
 260 265 270  
 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp  
 275 280 285  
 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu  
 290 295 300  
 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln  
 305 310 315 320  
 Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala  
 325 330 335  
 Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln  
 340 345 350  
 Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser  
 355 360 365  
 Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly  
 370 375 380  
 Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly  
 385 390 395 400  
 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg  
 405 410 415  
 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile  
 420 425 430  
 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg  
 435 440 445

Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val  
 450 455 460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile  
 465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr  
 485

<210> 699  
 <211> 1587  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1564)  
 <223> FRXA00483

<400> 699  
 agaccaaga gtaaaatccc aggatttgct tataacttgcg ctcatggata atcaacttcg 60

tcccactttg cattatcaag ctcaaaaccc gcaccggcga gtg ctg gtc acc ggt 115  
 Val Leu Val Thr Gly  
 1 5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163  
 Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala  
 10 15 20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211  
 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg  
 25 30 35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259  
 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp  
 40 45 50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307  
 Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr  
 55 60 65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355  
 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu  
 70 75 80 85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403  
 Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile  
 90 95 100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451  
 Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile  
 105 110 115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499  
 Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile  
 120 125 130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547  
 Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile

135	140	145	
att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu 150 155 160 165			595
cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu 170 175 180			643
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp 185 190 195			691
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser 200 205 210			739
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu 215 220 225			787
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu 230 235 240 245			835
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser 250 255 260			883
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His 265 270 275			931
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr 280 285 290			979
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val 295 300 305			1027
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly 310 315 320 325			1075
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val 330 335 340			1123
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile 345 350 355			1171
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp 360 365 370			1219
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly 375 380 385			1267

gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315  
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp  
 390 395 400 405  
 tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363  
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala  
 410 415 420  
 gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411  
 Glu-Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp  
 425 430 435  
 aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459  
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro  
 440 445 450  
 aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507  
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His  
 455 460 465  
 gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555  
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg  
 470 475 480 485  
 aaa ctc act taatcgcaga gtaggcgtct aaa 1587  
 Lys Leu Thr

&lt;210&gt; 700

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 700

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr  
 1 5 10 15  
 Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys  
 20 25 30  
 Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu  
 35 40 45  
 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val  
 50 55 60  
 Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp  
 65 70 75 80  
 Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala  
 85 90 95  
 Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro  
 100 105 110  
 Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu  
 115 120 125  
 Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu

130	135	140
Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile		
145	150	155 160
Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile		
	165	170 175
Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu		
	180	185 190
Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile		
	195	200 205
Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala		
	210	215 220
Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu		
	225	230 235 240
Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val		
	245	250 255
Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala		
	260	265 270
Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp		
	275	280 285
Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu		
	290	295 300
Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln		
	305	310 315 320
Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala		
	325	330 335
Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln		
	340	345 350
Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser		
	355	360 365
Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly		
	370	375 380
Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly		
	385	390 395 400
Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg		
	405	410 415
Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile		
	420	425 430
Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg		
	435	440 445
Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val		
	450	455 460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile  
 465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr  
 485

<210> 701

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> RXA01534

<400> 701

attgctctca tcggttcgat atagactgaa ttgtctaggt taatatccaa tatggaagaa 60

aaactagaca gttaagtaga ctgaatggcc tactaggtgc atg act tca gca atc 115  
 Met Thr Ser Ala Ile  
 1 5

acc acc gca act gat ctt cgc tcc gta ctg cga aac gta cca acc cca 163  
 Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg Asn Val Pro Thr Pro  
 10 15 20

att agc ttc att gca acc cac acc gat cag cct ctg ggc atg atc gtt 211  
 Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro Leu Gly Met Ile Val  
 25 30 35

ggg tca ttc gtc agc att agc gcc gaa cca cca ttg gta ggc atc ttc 259  
 Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro Leu Val Gly Ile Phe  
 40 45 50

ttg cag aag agc tct tct tca tgg cca gct atc gag cag gca tta gtt 307  
 Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile Glu Gln Ala Leu Val  
 55 60 65

acc ggc caa gag cta ggc att tct atc ctc ggc ggg gca cac gca gac 355  
 Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly Gly Ala His Ala Asp  
 70 75 80 85

cat gtg cgt aag ctt tct ggc cca tcc gac cag cgc ttt gaa aac ctt 403  
 His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln Arg Phe Glu Asn Leu  
 90 95 100

ggg tgg gca tcc acc gaa aac ggt gcg att cac ctt gaa ggc gct gat 451  
 Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His Leu Glu Gly Ala Asp  
 105 110 115

gca caa cta acc acg aaa ctt cat gat ctc cag gaa atc ggc gat cac 499  
 Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln Glu Ile Gly Asp His  
 120 125 130

ttc ttt gca gtt cta gaa gtt att gac gct tcc gct gac caa gac ttc 547  
 Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser Ala Asp Gln Asp Phe  
 135 140 145

agc tca gcg ctg gtg tac cac cgc tca cag gtg tcc tcg ctg 589  
 Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val Ser Ser Leu  
 150 155 160

taggacacta aattttaaga ggg 612

<210> 702

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

Met Thr Ser Ala Ile Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg  
 1 5 10 15

Asn Val Pro Thr Pro Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro  
 20 25 30

Leu Gly Met Ile Val Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro  
 35 40 45

Leu Val Gly Ile Phe Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile  
 50 55 60

Glu Gln Ala Leu Val Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly  
 65 70 75 80

Gly Ala His Ala Asp His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln  
 85 90 95

Arg Phe Glu Asn Leu Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His  
 100 105 110

Leu Glu Gly Ala Asp Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln  
 115 120 125

Glu Ile Gly Asp His Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser  
 130 135 140

Ala Asp Gln Asp Phe Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val  
 145 150 155 160

Ser Ser Leu

<210> 703

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> RXA00288

<400> 703

ggcgtgctaa aaaagcacgt caaatacaga atcggcagat tacatcgctg agcagagaaa 60

acacggggcat gaaacgtacc caagggctaa catcgggggc atg agc gcg caa atg 115



															Met	Ser	Ala	Gln	Met	
															1				5	
gat	acc	cct	gat	ccc	act	atg	tct	gct	gtt	gca	atg	tta	gat	tcc	atc	163				
Asp	Thr	Pro	Asp	Pro	Thr	Met	Ser	Ala	Val	Ala	Met	Leu	Asp	Ser	Ile					
				10					15					20						
cct	tct	gat	caa	cca	gat	ttc	ctg	atc	gat	gta	gaa	gta	gat	cga	cca	211				
Pro	Ser	Asp	Gln	Pro	Asp	Phe	Leu	Ile	Asp	Val	Glu	Val	Asp	Arg	Pro					
				25					30					35						
act	ccc	gga	cca	cat	gat	ctg	cta	gtc	cac	att	gag	gcg	gtc	tca	att	259				
Thr	Pro	Gly	Pro	His	Asp	Leu	Leu	Val	His	Ile	Glu	Ala	Val	Ser	Ile					
				40					45					50						
aac	cct	gtt	gat	acc	aag	gta	cgc	atg	cgg	gcc	ggg	aag	caa	aag	cat	307				
Asn	Pro	Val	Asp	Thr	Lys	Val	Arg	Met	Arg	Ala	Gly	Lys	Gln	Lys	His					
				55					60					65						
cct	aaa	att	tta	ggc	ttt	gat	gct	gca	ggc	gag	gtg	gtg	gct	gtt	gga	355				
Pro	Lys	Ile	Leu	Gly	Phe	Asp	Ala	Ala	Gly	Glu	Val	Val	Ala	Val	Gly					
				70					75					80						
tcg	cag	gtc	acg	ctc	ttc	aat	gtt	ggc	gac	aaa	gtg	ttc	tac	gca	gga	403				
Ser	Gln	Val	Thr	Leu	Phe	Asn	Val	Gly	Asp	Lys	Val	Phe	Tyr	Ala	Gly					
				90					95					100						
tcc	aat	cag	cgt	cca	gga	agt	aac	gca	gag	tac	cag	gtg	gtg	gat	gaa	451				
Ser	Asn	Gln	Arg	Pro	Gly	Ser	Asn	Ala	Glu	Tyr	Gln	Val	Val	Asp	Glu					
				105					110					115						
cgg	ctg	gtg	ggc	cac	gca	cca	caa	agc	ttg	ggg	gca	cac	gac	gcc	gct	499				
Arg	Leu	Val	Gly	His	Ala	Pro	Gln	Ser	Leu	Gly	Ala	His	Asp	Ala	Ala					
				120					125					130						
gct	ctc	cca	ctt	gtc	gcg	ctc	act	gca	tgg	gag	tca	ctt	ttt	gac	cga	547				
Ala	Leu	Pro	Leu	Val	Ala	Leu	Thr	Ala	Trp	Glu	Ser	Leu	Phe	Asp	Arg					
				135					140					145						
ttg	gga	gta	act	cag	tca	act	act	gga	aca	ctg	ttg	gtc	ttg	ggc	ggc	595				
Leu	Gly	Val	Thr	Gln	Ser	Thr	Thr	Gly	Thr	Leu	Leu	Val	Leu	Gly	Gly					
				150					155					160						
tca	gga	ggc	gtg	cct	tca	gct	ctt	att	caa	ctt	gct	cga	gct	ctc	act	643				
Ser	Gly	Gly	Val	Pro	Ser	Ala	Leu	Ile	Gln	Leu	Ala	Arg	Ala	Leu	Thr					
				170					175					180						
ggc	ctg	aaa	gta	gtg	gca	aca	gct	tct	cgc	cct	gaa	tca	caa	gaa	tgg	691				
Gly	Leu	Lys	Val	Val	Ala	Thr	Ala	Ser	Arg	Pro	Glu	Ser	Gln	Glu	Trp					
				185					190					195						
gtg	aca	aag	ctc	ggc	gct	cat	gag	gtg	att	gat	cac	tcc	aag	gat	ttg	739				
Val	Thr	Lys	Leu	Gly	Ala	His	Glu	Val	Ile	Asp	His	Ser	Lys	Asp	Leu					
				200					205					210						
agt	gag	caa	atc	tcc	gac	gtg	gat	ttt	gtt	ttc	agc	tcg	tgg	act	act	787				
Ser	Glu	Gln	Ile	Ser	Asp	Val	Asp	Phe	Val	Phe	Ser	Ser	Trp	Thr	Thr					
				215					220					225						
ggg	cgt	gaa	gta	gag	ctc	gcc	acg	ttg	atg	aaa	ccc	cag	tcc	cac	cta	835				
Gly	Arg	Glu	Val	Glu	Leu	Ala	Thr	Leu	Met	Lys	Pro	Gln	Ser	His	Leu					

230	235	240	245	
gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa				883
Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln	250	255	260	
aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc				931
Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe	265	270	275	
aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc				979
Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala	280	285	290	
gac atg gtt gat cgg ggt cag ttt gag tcc gtg aca gca acg gtg ctg				1027
Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu	295	300	305	
gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag				1075
Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu	310	315	320	325
cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac				1121
Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val	330	335		
ttgaaaaatg cac				1134
 <210> 704				
<211> 337				
<212> PRT				
<213> Corynebacterium glutamicum				
 <400> 704				
Met Ser Ala Gln Met Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala	1	5	10	15
Met Leu Asp Ser Ile Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val	20	25	30	
Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile	35	40	45	
Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala	50	55	60	
Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu	65	70	75	80
Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys	85	90	95	
Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr	100	105	110	
Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly	115	120	125	
Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu	130	135	140	

Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu  
 145 150 155 160  
 Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu  
 165 170 175  
 Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro  
 180 185 190  
 Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp  
 195 200 205  
 His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe  
 210 215 220  
 Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys  
 225 230 235 240  
 Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu  
 245 250 255  
 Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe  
 260 265 270  
 Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile  
 275 280 285  
 Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val  
 290 295 300  
 Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly  
 305 310 315 320  
 His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg  
 325 330 335  
 Val

<210> 705  
 <211> 1089  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1066)  
 <223> RXA02741

<400> 705  
 actggtcacc tggtttggtc tgcactctga ctccctcaa aagggcacaa tttggtcaat 60  
 ttcccaacct tgtctttcag tcatgggttag tgtgggaacc atg aag gca atc tta 115  
 Met Lys Ala Ile Leu  
 1 5  
 gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac 163  
 Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp  
 10 15 20

gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct 211  
 Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala  
 25 30 35

ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct 259  
 Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala  
 40 45 50

cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag 307  
 Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu  
 55 60 65

gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat 355  
 Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp  
 70 75 80 85

gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg 403  
 Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu  
 90 95 100

gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg 451  
 Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu  
 105 110 115

atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt 499  
 Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu  
 120 125 130

gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga 547  
 Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly  
 135 140 145

ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc 595  
 Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser  
 150 155 160 165

gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct 643  
 Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala  
 170 175 180

tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg 691  
 Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg  
 185 190 195

cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag 739  
 His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln  
 200 205 210

tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg 787  
 Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val  
 215 220 225

tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag 835  
 Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln  
 230 235 240 245

ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc 883  
 Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly  
 250 255 260

gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc 931  
 Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val 275  
 265 270 275

acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca 979  
 Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr 290  
 280 285 290

tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt 1027  
 Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg 305  
 295 300 305

agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca 1076  
 Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp 320  
 310 315 320

taaaaagatc ctg 1089

<210> 706  
 <211> 322  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 706  
 Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu  
 1 5 10 15

Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val  
 20 25 30

Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln  
 35 40 45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr  
 50 55 60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys  
 65 70 75 80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val  
 85 90 95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val  
 100 105 110

Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn  
 115 120 125

Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly  
 130 135 140

Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly  
 145 150 155 160

Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala  
 165 170 175

Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala  
 180 185 190

Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr  
 195 200 205  
 Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg  
 210 215 220  
 Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu  
 225 230 235 240  
 Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr  
 245 250 255  
 Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys  
 260 265 270  
 Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val  
 275 280 285  
 Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg  
 290 295 300  
 Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro  
 305 310 315 320  
 Lys Asp

<210> 707  
 <211> 990  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(967)  
 <223> RXN02560

<400> 707  
 ttgggggcaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60  
 ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg 115  
 Met Gln Gly Asn Ser  
 1 5  
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163  
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro  
 10 15 20  
 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211  
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro  
 25 30 35  
 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259  
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val  
 40 45 50  
 cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307  
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile  
 55 60 65

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att	355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile	
70 75 80 85	
tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg	403
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly	
90 95 100	
atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg	451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu	
105 110 115	
att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa	499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu	
120 125 130	
gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg	547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly	
135 140 145	
ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag	595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu	
150 155 160 165	
tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg	643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala	
170 175 180	
gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc	691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val	
185 190 195	
gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att	739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile	
200 205 210	
aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc	787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr	
215 220 225	
gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act	835
Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr	
230 235 240 245	
tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg	883
Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala	
250 255 260	
cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt	931
His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu	
265 270 275	
agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg	977
Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg	
280 285	
attatggacg cct	990

&lt;210&gt; 708

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 708

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys  
 1 5 10 15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro  
 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His  
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp  
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser  
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg  
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln  
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala  
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp  
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala  
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser  
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro  
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro  
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His  
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp  
 225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp  
 245 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr  
 260 265 270

Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu  
 275 280 285

Arg



<210> 709  
 <211> 922  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(922)  
 <223> FRXA02560

<400> 709

ttggggcaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60

ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg 115  
 Met Gln Gly Asn Ser  
 1 5

ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163  
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro  
 10 15 20

gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211  
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro  
 25 30 35

ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259  
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val  
 40 45 50

cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307  
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile  
 55 60 65

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355  
 Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile  
 70 75 80 85

tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403  
 Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly  
 90 95 100

atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451  
 Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu  
 105 110 115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499  
 Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu  
 120 125 130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547  
 Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly  
 135 140 145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595  
 Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu  
 150 155 160 165

tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg 643  
 Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala  
 170 175 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691  
 Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val  
                   185                                  190                                  195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739  
 Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile  
                   200                                  205                                  210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787  
 Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr  
                   215                                  220                                  225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835  
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr  
 230                                  235                                  240                                  245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883  
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala  
                   250                                  255                                  260

cat agg gcg gcg tct aaa cgc tgt tac aag aac caa gaa 922  
 His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn Gln Glu  
                   265                                  270

<210> 710

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys  
           1                                  5                                  10                                  15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro  
                   20                                  25                                  30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His  
           35                                  40                                  45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp  
           50                                  55                                  60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser  
           65                                  70                                  75                                  80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg  
                   85                                  90                                  95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln  
           100                                  105                                  110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala  
           115                                  120                                  125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp  
           130                                  135                                  140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala  
           145                                  150                                  155                                  160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser  
 165 170 175  
 Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro  
 180 185 190  
 Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro  
 195 200 205  
 Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His  
 210 215 220  
 Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp  
 225 230 235 240  
 Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp  
 245 250 255  
 Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn  
 260 265 270

Gln Glu

<210> 711

<211> 870

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(847)

<223> RXA01311

<400> 711

tcgtctccgc atgggaacca ggcgagaatg gaaccttcgt ctgccacgca gaaccactgt 60

tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt 115  
 Met Lys Leu Thr Leu  
 1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163  
 Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr  
 10 15 20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211  
 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu  
 25 30 35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259  
 Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala  
 40 45 50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307  
 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu  
 55 60 65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355  
 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala

70	75	80	85	
cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca				403
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro	90	95	100	
ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc				451
Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg	105	110	115	
tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac				499
Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn	120	125	130	
gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc				547
Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr	135	140	145	
gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt				595
Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys	150	155	160	165
gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag				643
Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys	170	175	180	
ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg				691
Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu	185	190	195	
cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc				739
Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys	200	205	210	
tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg				787
Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu	215	220	225	
acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga				835
Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg	230	235	240	245
ggc aaa gac gac tagtctttaa tccaagtaag tac				870
Gly Lys Asp Asp				

&lt;210&gt; 712

&lt;211&gt; 249

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 712

Met	Lys	Leu	Thr	Leu	Glu	Ile	Trp	Arg	Gln	Ala	Gly	Pro	Thr	Ala	Glu
1				5					10					15	

Gly	Lys	Phe	Glu	Thr	Val	Gln	Val	Asp	Asp	Ala	Val	Ala	Gln	Met	Ser
			20					25					30		

Ile	Leu	Glu	Leu	Leu	Asp	His	Val	Asn	Asn	Lys	Phe	Ile	Glu	Glu	Gly
	35						40					45			

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly  
 50 55 60  
 Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn  
 65 70 75 80  
 Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr  
 85 90 95  
 Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp  
 100 105 110  
 Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly  
 115 120 125  
 Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His  
 130 135 140  
 Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile  
 145 150 155 160  
 Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu  
 165 170 175  
 Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys  
 180 185 190  
 Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr  
 195 200 205  
 Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro  
 210 215 220  
 Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala  
 225 230 235 240  
 Arg Ala Ala Phe Arg Gly Lys Asp Asp  
 245

<210> 713  
 <211> 929  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(906)  
 <223> RXN03014

<400> 713  
 tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc 48  
 Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr  
 1 5 10 15  
 ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg 96  
 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met  
 20 25 30  
 gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt 144

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val	
35 40 45	
tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg	192
Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met	
50 55 60	
gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc	240
Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu	
65 70 75 80	
gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg	288
Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu	
85 90 95	
ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca	336
Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala	
100 105 110	
ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg	384
Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser	
115 120 125	
att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca	432
Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala	
130 135 140	
ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat	480
Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp	
145 150 155 160	
atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg	528
Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met	
165 170 175	
atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc	576
Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile	
180 185 190	
ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg	624
Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val	
195 200 205	
gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt	672
Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu	
210 215 220	
gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc	720
Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile	
225 230 235 240	
ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc	768
Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly	
245 250 255	
aag atc atg ctc atc gaa gcc gcc gcc cga aga tgg cag ttg gct ggc	816
Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly	
260 265 270	
atg ggt cct tat cgc agg cgc cgt tgt cac ctc act gct cac ctt gta	864
Met Gly Pro Tyr Arg Arg Arg Arg Cys His Leu Thr Ala His Leu Val	

275 280 285  
 cac cat ggt tct ggt ctg gtc caa ggc ctt ctg gcg cga ccg 906  
 His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro  
 290 295 300

taaagacgcc cccgatggag caa 929

<210> 714

<211> 302

<212> PRT

<213> Corynebacterium glutamicum

<400> 714

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr  
 1 5 10 15

Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met  
 20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val  
 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met  
 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu  
 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu  
 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala  
 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser  
 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala  
 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp  
 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met  
 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile  
 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val  
 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu  
 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile  
 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly

145	150	155	160	
atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met	165	170	175	528
atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile	180	185	190	576
ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val	195	200	205	624
gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu	210	215	220	672
gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile	225	230	235	720
ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc Pro Ala Ile Asn Leu Gly Gly Ile Pro Phe Ser Gly Phe Leu Gly	245	250	255	768
aag atc atg ctc atc gaa gcc ggc gcc gaa gat ggc agt tgg ctg gca Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala	260	265	270	816
tgg gtc ctt atc gca ggc gcc gtt gtc acc tca ctg ctc acc ttg tac Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr	275	280	285	864
acc atg gtt ctg gtc tgg tcc aag gcc ttc tgg cgc gac cgt aaa gac Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp	290	295	300	912
gcc ccc gat gga gca acc gca ctt gcg cga ccc gca cct ttg gta gat Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp	305	310	315	960
gtc caa gac gaa gtc gcc gtt aaa gac cgc aac gat gtc gga cgg atg Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met	325	330	335	1008
cct tgg ggc atg gtc ttc tcc act gct ctc ctg gtt tca gca tct ctt Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu	340	345	350	1056
gct gta tcc gtg ctc gca gga cca ctg tca tct att act gga cgc gcc Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala	355	360	365	1104
gcc gaa tcc gca caa gat gtc aac atc tac cgc gcc gca gta ctc ggc Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly	370	375	380	1152
ccc aac tac ctc gac cca tca cgc aca ctc gag atg gag cgt tac gac Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp	385	390	395	1200
			400	



	245		250		255
Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly					
	260		265		270
Met Gly Pro Tyr Arg Arg Arg Arg Cys His Leu Thr Ala His Leu Val					
	275		280		285
His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro					
	290		295		300

<210> 715  
 <211> 1280  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1257)  
 <223> FRXA00910

<400> 715

tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc	48
Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr	
1 5 10 15	
ttg ggt gca tcg ccg gca cgt gta cgt tcc gcc gtg ggt tac gtg atg	96
Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met	
20 25 30	
gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt	144
Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val	
35 40 45	
tac gcc tca gtg ggc acg ttg aac atg gct cac gtt gcc cta cgc atg	192
Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met	
50 55 60	
gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc	240
Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu	
65 70 75 80	
gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg	288
Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu	
85 90 95	
ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca	336
Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala	
100 105 110	
ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg	384
Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser	
115 120 125	
att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca	432
Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala	
130 135 140	
ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat	480
Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp	

gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag 1248  
 Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu  
                   405                  410                  415

gac caa cca tgatcagtg attcaaacga cga 1280  
 Asp Gln Pro

<210> 716

<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 716

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr  
   1                  5                  10                  15

Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met  
                   20                  25                  30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val  
                   35                  40                  45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met  
   50                  55                  60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu  
   65                  70                  75                  80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu  
                   85                  90                  95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala  
                   100                  105                  110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser  
   115                  120                  125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala  
   130                  135                  140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp  
   145                  150                  155                  160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met  
                   165                  170                  175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile  
                   180                  185                  190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val  
                   195                  200                  205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu  
   210                  215                  220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile  
   225                  230                  235                  240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly  
 245 250 255

Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala  
 260 265 270

Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr  
 275 280 285

Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp  
 290 295 300

Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp  
 305 310 315 320

Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met  
 325 330 335

Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu  
 340 345 350

Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala  
 355 360 365

Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly  
 370 375 380

Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp  
 385 390 395 400

Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu  
 405 410 415

Asp Gln Pro

<210> 717  
 <211> 1051  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1051)  
 <223> RXN01895

<400> 717  
 cgcgtagacg tgctcaacac gacaacgctt aaacggctgc acgcgtaaca cggcagaccg 60

cacaagcttt aagatccacg atcaggagac tttgacaaat atg tca gtt aac cca 115  
 Met Ser Val Asn Pro  
 1 5

acc cgc ccc gaa ggc ggc cgt cac cac gtc gtc gtc atc ggt tct ggt 163  
 Thr Arg Pro Glu Gly Arg His His Val Val Val Ile Gly Ser Gly  
 10 15 20

ttt ggt ggc ctt ttt gct gcc aag aac ctg gcc aag gca gac gtc gat 211  
 Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala Lys Ala Asp Val Asp  
 25 30 35

gtc act ctg att gac cgc acc aac cac cac ctc ttc cag cca ctg ctg	259
Val Thr Leu Ile Asp Arg Thr Asn His His Leu Phe Gln Pro Leu Leu	
40 45 50	
tac caa gtg gca acc ggt atc ctc tcc tcc ggt gaa atc gca cct tcc	307
Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly Glu Ile Ala Pro Ser	
55 60 65	
act cga cag atc ctg ggc tcc cag gaa aac gtc aac gtc atc aag ggc	355
Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val Asn Val Ile Lys Gly	
70 75 80 85	
gaa gtc acc gac atc aac gtc gag tcc cag act gtg acc gcc tcc ctg	403
Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr Val Thr Ala Ser Leu	
90 95 100	
ggc gag ttc acc cgc gtt ttt gag tac gat tcc ttg gtc gtt ggt gct	451
Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser Leu Val Val Gly Ala	
105 110 115	
ggc gca ggt cag tcc tac ttc ggc aat gat cac ttc gct gag ttc gca	499
Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His Phe Ala Glu Phe Ala	
120 125 130	
cct ggc atg aag tcc atc gac gat gca ctg gag att cgt gca cgc atc	547
Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu Ile Arg Ala Arg Ile	
135 140 145	
atc ggt gct ttc gag cgc gct gag atc tgc gag gat cca gct gag cgc	595
Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu Asp Pro Ala Glu Arg	
150 155 160 165	
gaa cgc ctg ctc acc ttc gtc gtt gtt ggc gct ggc cca acc ggt gtt	643
Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala Gly Pro Thr Gly Val	
170 175 180	
gag ctt gct ggc cag ttg gct gag atg gct cac cgc acc ctt gct ggt	691
Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His Arg Thr Leu Ala Gly	
185 190 195	
gag tac aag aac ttc aac acc aac tcc gca aag atc atc ctg ctt gat	739
Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp	
200 205 210	
ggt gct cca cag gtt ctt cct cca ttc ggt aag cgc cta ggc cgc aac	787
Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys Arg Leu Gly Arg Asn	
215 220 225	
gca cag cgc acc ctg gaa aag atg ggt gtc aac gtt cgc ctg aac gct	835
Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala	
230 235 240 245	
atg gtc acc aac gtt gac gct acc tcg gtc acc tac aag acc aag gac	883
Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp	
250 255 260	
ggc gaa gag cac acc atc gaa tct ttc tgc aag att tgg tcc gct ggt	931
Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly	
265 270 275	

ggt gcg gca tcc cca ctg ggc aag ctc gtc gca gag cag acc ggt gtt 979  
Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val  
280 285 290

gag acc gac cgc gca ggc cgc gtc atg gtt aac gat gac ctg tct gtt 1027  
Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val  
295 300 305

ggc gat cag aag aac gtc ttc gtt 1051  
Gly Asp Gln Lys Asn Val Phe Val  
310 315

<210> 718

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 718

Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val  
1 5 10 15

Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala  
20 25 30

Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu  
35 40 45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly  
50 55 60

Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val  
65 70 75 80

Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr  
85 90 95

Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser  
100 105 110

Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His  
115 120 125

Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu  
130 135 140

Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu  
145 150 155 160

Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala  
165 170 175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His  
180 185 190

Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys  
195 200 205

Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys  
210 215 220

Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn  
 225 230 235 240

Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr  
 245 250 255

Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys  
 260 265 270

Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala  
 275 280 285

Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn  
 290 295 300

Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val  
 305 310 315

<210> 719  
 <211> 816  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(816)  
 <223> FRXA01895

<400> 719

cac cac ctc ttc cag cca ctg ctg tac caa gtg gca acc ggt atc ctc	48
His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu	
1 5 10 15	
tcc tcc ggt gaa atc gca cct tcc act cga cag atc ctg ggc tcc cag	96
Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln	
20 25 30	
gaa aac gtc aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag	144
Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu	
35 40 45	
tcc cag act gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag	192
Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu	
50 55 60	
tac gat tcc ttg gtc gtt ggt gct ggc gca ggt cag tcc tac ttc ggc	240
Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly	
65 70 75 80	
aat gat cac ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat	288
Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp	
85 90 95	
gca ctg gag att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag	336
Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu	
100 105 110	
atc tgc gag gat cca gct gag cgc gaa cgc ctg ctc acc ttc gtc gtt	384
Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val	
115 120 125	

gtt ggc gct ggc cca acc ggt gtt gag ctt gct ggc cag ttg gct gag 432  
 Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu  
 130 135 140

atg gct cac cgc acc ctt gct ggt gag tac aag aac ttc aac acc aac 480  
 Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn  
 145 150 155 160

tcc gca aag atc atc ctg ctt gat ggt gct cca cag gtt ctt cct cca 528  
 Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro  
 165 170 175

ttc ggt aag cgc cta ggc cgc aac gca cag cgc acc ctg gaa aag atg 576  
 Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met  
 180 185 190

ggt gtc aac gtt cgc ctg aac gct atg gtc acc aac gtt gac gct acc 624  
 Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr  
 195 200 205

tcg gtc acc tac aag acc aag gac ggc gaa gag cac acc atc gaa tct 672  
 Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser  
 210 215 220

ttc tgc aag att tgg tcc gct ggt gtt gcg gca tcc cca ctg ggc aag 720  
 Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys  
 225 230 235 240

ctc gtc gca gag cag acc ggt gtt gag acc gac cgc gca ggc cgc gtc 768  
 Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val  
 245 250 255

atg gtt aac gat gac ctg tct gtt ggc gat cag aag aac gtc ttc gtt 816  
 Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val  
 260 265 270

&lt;210&gt; 720

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 720

His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu  
 1 5 10 15

Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln  
 20 25 30

Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu  
 35 40 45

Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu  
 50 55 60

Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly  
 65 70 75 80

Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp  
 85 90 95

Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu  
 100 105 110

Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val  
 115 120 125

Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu  
 130 135 140

Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn  
 145 150 155 160

Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro  
 165 170 175

Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met  
 180 185 190

Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr  
 195 200 205

Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser  
 210 215 220

Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys  
 225 230 235 240

Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val  
 245 250 255

Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val  
 260 265 270

<210> 721  
 <211> 2409  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2386)  
 <223> RXA00703

<400> 721  
 ctgggagtcc tcttgatttt aggttttcca cataccccca tatagattga agaattcatt 60  
 tttcggcatg ggttcaattg ccgggtctag actgtgacct atg aca acc cct cca 115  
 Met Thr Thr Pro Pro  
 1 5

act gag att tcg aac gtg aat ccc acc gcg aat gaa ttt gat gat ccg 163  
 Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn Glu Phe Asp Asp Pro  
 10 15 20

gat gtg gga cgg cgc att act tct gct gct ggt gtg cca ggc gtt ttg 211  
 Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly Val Pro Gly Val Leu



25										30					35					
cat	gcg	ctc	cag	cat	gct	gtt	ccg	aat	cgt	gcc	ctg	ctg	ccg	ttg	ctc	259				
His	Ala	Leu	Gln	His	Ala	Val	Pro	Asn	Arg	Ala	Leu	Leu	Pro	Leu	Leu					
40						45			50											
acc	atg	aat	aaa	cca	ggc	ggc	atc	gac	tgt	cct	ggg	tgt	gct	tgg	cct	307				
Thr	Met	Asn	Lys	Pro	Gly	Gly	Ile	Asp	Cys	Pro	Gly	Cys	Ala	Trp	Pro					
55			60			65														
gag	cct	tcc	act	gcc	aac	ctt	ggg	gtg	gtt	gag	ttc	tgc	gag	aac	ggg	355				
Glu	Pro	Ser	Thr	Ala	Asn	Leu	Gly	Val	Val	Glu	Phe	Cys	Glu	Asn	Gly					
70				75			80			85										
gcc	aag	gcg	gtc	gcc	gag	gaa	aca	aca	cct	gat	cgt	gcc	ggc	aaa	gag	403				
Ala	Lys	Ala	Val	Ala	Glu	Glu	Thr	Thr	Pro	Asp	Arg	Ala	Gly	Lys	Glu					
			90			95			100											
ttc	tgg	gca	gag	cat	tct	att	tat	gat	ctg	cgg	gaa	aag	acc	gat	cac	451				
Phe	Trp	Ala	Glu	His	Ser	Ile	Tyr	Asp	Leu	Arg	Glu	Lys	Thr	Asp	His					
105			110			115														
tgg	ctg	gga	aag	cgt	ggc	cga	atc	acc	gag	ccc	atg	ttt	tat	gat	cgt	499				
Trp	Leu	Gly	Lys	Arg	Gly	Arg	Ile	Thr	Glu	Pro	Met	Phe	Tyr	Asp	Arg					
120			125			130														
tct	tct	ggc	gat	gat	cac	tac	cgc	cct	att	tct	tgg	gat	cgt	gca	ttt	547				
Ser	Ser	Gly	Asp	Asp	His	Tyr	Arg	Pro	Ile	Ser	Trp	Asp	Arg	Ala	Phe					
135			140			145														
gcg	atc	att	gcg	tcg	aag	ctc	cgc	gag	atc	gag	cca	gat	gaa	gcg	gtg	595				
Ala	Ile	Ile	Ala	Ser	Lys	Leu	Arg	Glu	Ile	Glu	Pro	Asp	Glu	Ala	Val					
150				155			160			165										
ttt	tac	acc	tct	ggg	cga	gca	ccc	aat	gag	ccg	gct	tat	atg	ctg	cag	643				
Phe	Tyr	Thr	Ser	Gly	Arg	Ala	Pro	Asn	Glu	Pro	Ala	Tyr	Met	Leu	Gln					
170			175			180														
ctt	cta	gcc	cgc	cga	ctt	ggc	aca	aat	aat	ctt	cca	gac	tgt	gga	aac	691				
Leu	Leu	Ala	Arg	Arg	Leu	Gly	Thr	Asn	Asn	Leu	Pro	Asp	Cys	Gly	Asn					
185			190			195														
atg	tgc	cac	gag	tcc	acc	ggg	act	gcc	ttg	ggg	gag	acc	ttg	ggg	ttg	739				
Met	Cys	His	Glu	Ser	Thr	Gly	Thr	Ala	Leu	Gly	Glu	Thr	Leu	Gly	Leu					
200			205			210														
ggc	aag	gga	tcc	gtg	gtg	atg	gag	gat	ttc	tac	aac	act	gat	ttg	ttg	787				
Gly	Lys	Gly	Ser	Val	Val	Met	Glu	Asp	Phe	Tyr	Asn	Thr	Asp	Leu	Leu					
215			220			225														
att	tcc	gtg	gga	caa	aac	ccg	ggc	acc	aac	cac	cca	cgt	gcg	ttg	acg	835				
Ile	Ser	Val	Gly	Gln	Asn	Pro	Gly	Thr	Asn	His	Pro	Arg	Ala	Leu	Thr					
230				235			240			245										
gct	ttc	aaa	gaa	ttg	aag	gaa	aac	ggg	ggc	aag	att	ctg	gcg	ctg	aac	883				
Ala	Phe	Lys	Glu	Leu	Lys	Glu	Asn	Gly	Gly	Lys	Ile	Leu	Ala	Leu	Asn					
250			255			260														
ccc	atg	cca	gag	acc	ggg	ctg	atg	aaa	ttc	cgt	gag	ccc	caa	tca	gtc	931				
Pro	Met	Pro	Glu	Thr	Gly	Leu	Met	Lys	Phe	Arg	Glu	Pro	Gln	Ser	Val					
265			270			275														

aag ggc gcg ttg agc att tca gac aaa ctt gct gat gaa tac ttg cag Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala Asp Glu Tyr Leu Gln 280 285 290	979
atc cgt ctt gat gga gac cgc gca ttc ttc cag gcg ctc aac aag gaa Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln Ala Leu Asn Lys Glu 295 300 305	1027
ctc atc cgt aga gat gcc cta gat cat gca ttc ttg gat aaa ttc tgt Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe Leu Asp Lys Phe Cys 310 315 320 325	1075
tca ggt gtg gat gaa acc atc gag cac ctc aaa tca ctc gat gat gag Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys Ser Leu Asp Asp Glu 330 335 340	1123
gtt ctg ctc aag gga tgc ggt ctg acg gca gcg gag atc aac aag gcc Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala Glu Ile Asn Lys Ala 345 350 355	1171
gct gac atg gtg gaa aag tct gac acc gtg gtg gtg tca tgg act ctc Ala Asp Met Val Glu Lys Ser Asp Thr Val Val Val Ser Trp Thr Leu 360 365 370	1219
ggg gtc acc cag cat aag aac gct gtg tac acc atc cgt gaa atg gtg Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr Ile Arg Glu Met Val 375 380 385	1267
aac ttc ctg ctg ctt act gga aat att ggt aag cct ggc gca ggc act Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys Pro Gly Ala Gly Thr 390 395 400 405	1315
gcc ccg ctt cgt ggg cac tca aac gtc cag ggt gat cga acc atg ggt Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly Asp Arg Thr Met Gly 410 415 420	1363
att tgg gag aaa atg ccg gag gca ttc ctt gct gct ctt gaa aac gag Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu 425 430 435	1411
ttt ggt ttc gat gtg ccc cgc aag cac ggc ttc gac acg gta aat tcc Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe Asp Thr Val Asn Ser 440 445 450	1459
ctg cga gcc atg cgc gaa ggc aag acc aag ttc ttt ctc tcc ctc ggt Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe Phe Leu Ser Leu Gly 455 460 465	1507
ggc aac ctt gtt cga gtg tcc tca gat acg tct gtt gtc gaa aag ggc Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser Val Val Glu Lys Gly 470 475 480 485	1555
atg gaa tcc aat gag ctg acg gtg cat ctg tcg acc aag ccc aat ggt Met Glu Ser Asn Glu Leu Thr Val His Leu Ser Thr Lys Pro Asn Gly 490 495 500	1603
tca caa gca tgg cct ggt gag cag tca ctt atc ctt ccg gtg att gct Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile Leu Pro Val Ile Ala 505 510 515	1651

cga aca gat aag gat gtc caa aag tca ggc gtc cag cgt gtg aca gtt	1699
Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val Gln Arg Val Thr Val	
520 525 530	
gag gat tct gcc ggc gct gtt cac gca tcc act ggt aaa cga acc gcc	1747
Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr Gly Lys Arg Thr Ala	
535 540 545	
aac aag gat ctg aat ttg aag tcc gaa tgc gac atc att gga acc atc	1795
Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp Ile Ile Gly Thr Ile	
550 555 560 565	
ggg aag cag acc ttc ggt gat gcc ttc tgg cag ccg atg att gat aac	1843
Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln Pro Met Ile Asp Asn	
570 575 580	
tac gat gtg gtc cgc gat cac atc gag gcc acc att cct ggg ttc cac	1891
Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr Ile Pro Gly Phe His	
585 590 595	
gat ttc aac cgt cgc atc gac aac ccc ggt gga ttc ctc ctc ccc aac	1939
Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly Phe Leu Leu Pro Asn	
600 605 610	
gga cct cgt gag cgc atc ttc aac aca tcc aat ggc aag gcc caa ttg	1987
Gly Pro Arg Glu Arg Ile Phe Asn Thr Ser Asn Gly Lys Ala Gln Leu	
615 620 625	
acg gtt aat gaa acc aat gtg att gag cta ccc aag gac tat ttg ctt	2035
Thr Val Asn Glu Thr Asn Val Ile Glu Leu Pro Lys Asp Tyr Leu Leu	
630 635 640 645	
atg aac acg gta cgt tca cat gat caa tac aac tcc acg att tac ggt	2083
Met Asn Thr Val Arg Ser His Asp Gln Tyr Asn Ser Thr Ile Tyr Gly	
650 655 660	
ctg gat gac cgc tac cgc ggt gtt cgc aat ggt cgc cgc gta gtg ttc	2131
Leu Asp Asp Arg Tyr Arg Gly Val Arg Asn Gly Arg Arg Val Val Phe	
665 670 675	
gtc aat cct caa gat tgt aag caa cgt ggt ctc aag gat gga gac atc	2179
Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu Lys Asp Gly Asp Ile	
680 685 690	
gtc gat atc gtc tct gtc ttt gat gat ggc gaa cgc cga gca ccg aat	2227
Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu Arg Arg Ala Pro Asn	
695 700 705	
ttc cga gtg gtg gaa tat gac acc gcg agg gac tgc gtc acc acg tat	2275
Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp Cys Val Thr Thr Tyr	
710 715 720 725	
ttc cct gag gcc aac gta ttg gtt cca ttg gat tca gta gct gaa aaa	2323
Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp Ser Val Ala Glu Lys	
730 735 740	
tcc aac act cca gtg tcc aag tca gtt gtg gtt cgc ctt gaa gca aca	2371
Ser Asn Thr Pro Val Ser Lys Ser Val Val Val Arg Leu Glu Ala Thr	
745 750 755	
gga cgt act gct tct tagaaaaaca ccagggaatt ttc	2409

Gly Arg Thr Ala Ser  
760

<210> 722

<211> 762

<212> PRT

<213> Corynebacterium glutamicum

<400> 722

Met Thr Thr Pro Pro Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn  
1 5 10 15  
Glu Phe Asp Asp Pro Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly  
20 25 30  
Val Pro Gly Val Leu His Ala Leu Gln His Ala Val Pro Asn Arg Ala  
35 40 45  
Leu Leu Pro Leu Leu Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro  
50 55 60  
Gly Cys Ala Trp Pro Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu  
65 70 75 80  
Phe Cys Glu Asn Gly Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp  
85 90 95  
Arg Ala Gly Lys Glu Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg  
100 105 110  
Glu Lys Thr Asp His Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro  
115 120 125  
Met Phe Tyr Asp Arg Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser  
130 135 140  
Trp Asp Arg Ala Phe Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu  
145 150 155 160  
Pro Asp Glu Ala Val Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro  
165 170 175  
Ala Tyr Met Leu Gln Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu  
180 185 190  
Pro Asp Cys Gly Asn Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly  
195 200 205  
Glu Thr Leu Gly Leu Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr  
210 215 220  
Asn Thr Asp Leu Leu Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His  
225 230 235 240  
Pro Arg Ala Leu Thr Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys  
245 250 255  
Ile Leu Ala Leu Asn Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg  
260 265 270

Glu Pro Gln Ser Val Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala  
 275 280 285  
 Asp Glu Tyr Leu Gln Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln  
 290 295 300  
 Ala Leu Asn Lys Glu Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe  
 305 310 315 320  
 Leu Asp Lys Phe Cys Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys  
 325 330 335  
 Ser Leu Asp Asp Glu Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala  
 340 345 350  
 Glu Ile Asn Lys Ala Ala Asp Met Val Glu Lys Ser Asp Thr Val Val  
 355 360 365  
 Val Ser Trp Thr Leu Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr  
 370 375 380  
 Ile Arg Glu Met Val Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys  
 385 390 395 400  
 Pro Gly Ala Gly Thr Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly  
 405 410 415  
 Asp Arg Thr Met Gly Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala  
 420 425 430  
 Ala Leu Glu Asn Glu Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe  
 435 440 445  
 Asp Thr Val Asn Ser Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe  
 450 455 460  
 Phe Leu Ser Leu Gly Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser  
 465 470 475 480  
 Val Val Glu Lys Gly Met Glu Ser Asn Glu Leu Thr Val His Leu Ser  
 485 490 495  
 Thr Lys Pro Asn Gly Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile  
 500 505 510  
 Leu Pro Val Ile Ala Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val  
 515 520 525  
 Gln Arg Val Thr Val Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr  
 530 535 540  
 Gly Lys Arg Thr Ala Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp  
 545 550 555 560  
 Ile Ile Gly Thr Ile Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln  
 565 570 575  
 Pro Met Ile Asp Asn Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr  
 580 585 590  
 Ile Pro Gly Phe His Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly

1032

gat att gag ttg gtg cat ggc ctc ctc ttg tca gaa ggt ctg atc acg	307
Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr	
55 60 65	
gat gct tct gag gtt ttt acc gcc cgc tat tgt gca gga gct gtt ggc	355
Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly	
70 75 80 85	
cca gat aat caa aat acg tac aac gtc tta gaa ctt gat gtc atc ccc	403
Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro	
90 95 100	
aaa gac aat ccg gcc cgg gat ccc gtc cag aat ccc tcc cat aat ccc	451
Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro	
105 110 115	
gaa ggc agc caa cac gaa gca ctc cac atc cca act ttc caa ccg gta	499
Glu Gly Ser Gln His Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val	
120 125 130	
cgc gaa cta aac ctc gtg gca gcc caa cgc aat gtg ctg act acg tct	547
Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser	
135 140 145	
gct tgt ggt gtt tgt ggc acg acg tct att gag cag ttg atg aac aag	595
Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys	
150 155 160 165	
aag ggc tgg ccc att acg ccg att aca ccg gat cct cgg atg att gtg	643
Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val	
170 175 180	
tcg ttg cca gat aag ttg aag tcg aag cag aag att ttc gac aaa act	691
Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr	
185 190 195	
ggt ggg gtt cat gct gct ggt ttg gcc acg ctt gat ggt gag atg ttg	739
Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu	
200 205 210	
att att cga gag gat gtc ggt cgg cat aac gca gct gac aaa gtt ata	787
Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala Ala Asp Lys Val Ile	
215 220 225	
gga aac atg ctg atg gcg gga aag ctc ccc ttg gaa aac act att ttg	835
Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu	
230 235 240 245	
gtg atg agt tct agg gcg tct ttt gag ctt gtc caa aag gct gcc atg	883
Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met	
250 255 260	
gct gga att tcg ggt gta atc gct gtt ggt gct gca aca tcg ctg gca	931
Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala	
265 270 275	
atc gag gcg gcg cag gat tca ggt att ttc ctt gct ggt ttt gtt cgg	979
Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg	
280 285 290	

ggc aac aag ttt aac cac tat gcg ggc gag ctc gga taatgccaga 1025  
 Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu Gly  
 295 300 305

acaggtagaa cag 1038

<210> 724

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 724

Met Gly Arg Ile Thr Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr  
 1 5 10 15

Asp Glu Gln Val Phe Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu  
 20 25 30

Glu Pro Leu Glu Ile Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met  
 35 40 45

Arg Thr Pro Gly His Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser  
 50 55 60

Glu Gly Leu Ile Thr Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys  
 65 70 75 80

Ala Gly Ala Val Gly Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu  
 85 90 95

Leu Asp Val Ile Pro Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn  
 100 105 110

Pro Ser His Asn Pro Glu Gly Ser Gln His Glu Ala Leu His Ile Pro  
 115 120 125

Thr Phe Gln Pro Val Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn  
 130 135 140

Val Leu Thr Thr Ser Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu  
 145 150 155 160

Gln Leu Met Asn Lys Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp  
 165 170 175

Pro Arg Met Ile Val Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys  
 180 185 190

Ile Phe Asp Lys Thr Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu  
 195 200 205

Asp Gly Glu Met Leu Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala  
 210 215 220

Ala Asp Lys Val Ile Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu  
 225 230 235 240

Glu Asn Thr Ile Leu Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val  
 245 250 255



Gln Lys Ala Ala Met Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala  
 260 265 270

Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu  
 275 280 285

Ala Gly Phe Val Arg Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu  
 290 295 300

Gly  
 305

<210> 725  
 <211> 908  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(885)  
 <223> FRXA00705

<400> 725  
 cca cgc gtt gtg tcc act gac gag caa gtt ttt gtt aac act cgt ccg 48  
 Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro  
 1 5 10 15

gat act gtt gcg gtg gag gag cct cta gaa att cgg gtt aat ggc act 96  
 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr  
 20 25 30

gcg ctt acc acc act atg cgc acg ccc ggc cat gat att gag ttg gtg 144  
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val  
 35 40 45

cat ggc ctc ctc ttg tca gaa ggt ctg atc acg gat gct tct gag gtt 192  
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val  
 50 55 60

ttt acc gcc cgc tat tgt gca gga gct gtt ggc cca gat aat caa aat 240  
 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn  
 65 70 75 80

acg tac aac gtc tta gaa ctt gat gtc atc ccc aaa gac aat ccg gcc 288  
 Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala  
 85 90 95

cgg gat ccc gtc cag aat ccc tcc cat aat ccc gaa ggc agc caa cac 336  
 Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His  
 100 105 110

gaa gca ctc cac atc cca act ttc caa ccg gta cgc gaa cta aac ctc 384  
 Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu  
 115 120 125

gtg gca gcc caa cgc aat gtg ctg act acg tct gct tgt ggt gtt tgt 432  
 Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys  
 130 135 140

ggc acg acg tct att gag cag ttg atg aac aag aag ggc tgg ccc att 480

Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile  
 145 150 155 160  
 acg ccg att aca ccg gat cct cgg atg att gtg tcg ttg cca gat aag 528  
 Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys  
 165 170 175  
 ttg aag tcg aag cag aag att ttc gac aaa act ggt ggg gtt cat gct 576  
 Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala  
 180 185 190  
 gct ggt ttg gcc acg ctt gat ggt gag atg ttg att att cga gag gat 624  
 Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp  
 195 200 205  
 gtc ggt cgg cat aac gca gct gac aaa gtt ata gga aac atg ctg atg 672  
 Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met  
 210 215 220  
 gcg gga aag ctc ccc ttg gaa aac act att ttg gtg atg agt tct agg 720  
 Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg  
 225 230 235 240  
 gcg tct ttt gag ctt gtc caa aag gct gcc atg gct gga att tcg ggt 768  
 Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly  
 245 250 255  
 gta atc gct gtt ggt gct gca aca tcg ctg gca atc gag gcg gcg cag 816  
 Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln  
 260 265 270  
 gat tca ggt att ttc ctt gct ggt ttt gtt cgg ggc aac aag ttt aac 864  
 Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn  
 275 280 285  
 cac tat gcg ggc gag ctc gga taatgccaga acaggtagaa cag 908  
 His Tyr Ala Gly Glu Leu Gly  
 290 295

&lt;210&gt; 726

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 726

Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro  
 1 5 10 15  
 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr  
 20 25 30  
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val  
 35 40 45  
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val  
 50 55 60  
 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn  
 65 70 75 80

```

<400> 727
gaagagtact tgcaccacga cgactaacac cgcaatttaa aggcttttca agcctgcccc 60

acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac 115
                               Met Leu Pro Val Asn
                               1           5

caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc 163

```

Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile	
10 15 20	
atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa	211
Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln	
25 30 35	
caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc	259
Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu	
40 45 50	
gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac	307
Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp	
55 60 65	
atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa	355
Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu	
70 75 80 85	
acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc	403
Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly	
90 95 100	
gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc	451
Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser	
105 110 115	
cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc	499
Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu	
120 125 130	
ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc	547
Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg	
135 140 145	
gtg gta tgg cca tgg atc ctc acc cca atg ctg gca ctg ctc ttc tac	595
Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu Ala Leu Leu Phe Tyr	
150 155 160 165	
ggt ggc acc cag ctg tac tcc gac gca gca cca gtc gtt cca gca ctg	643
Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro Val Val Pro Ala Leu	
170 175 180	
cag tcc ttc tgg ttc ccg atc cac gtt tcc tcc gtc tcc atc ggc gca	691
Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser Val Ser Ile Gly Ala	
185 190 195	
tcc atc ggt atc gtc tcc ggt att gca tcc ctg ctg tac ata ctg cgc	739
Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu Leu Tyr Ile Leu Arg	
200 205 210	
atg tgg caa cca aag ggt aaa gaa aag ggc ttc ttc ggc gca gta gca	787
Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe Phe Gly Ala Val Ala	
215 220 225	
aaa cca ctc cca tcc gga aaa acc ctg gat aac ctg gca tac aag acc	835
Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn Leu Ala Tyr Lys Thr	
230 235 240 245	
gcg atc tgg act gtc cca atc ttc ggc ctg ggc atc atc ttg ggt gcc	883
Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly Ile Ile Leu Gly Ala	

250	255	260	
atc tgg gca gaa gca gcc tgg ggt cgt ttc tgg gga tgg gat cct aag			931
Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys			
265	270	275	
gaa aca gtc tcc ttc atc acc tgg gtt ctc tac gct ggt tac ctc cac			979
Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His			
280	285	290	
gca cgt gca act gct ggt tgg cgc aac acc aac gct gca tgg atc aac			1027
Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn			
295	300	305	
atc ctg gcg ctg gtc acg atg att ttt aat ctg ttc ttc atc aac atg			1075
Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met			
310	315	320	325
gtc gta tct ggt ctg cac tct tac gcc gga ctg aac taagcacttt			1121
Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu Asn			
330	335		
tggttggcgg ggt			1134

&lt;210&gt; 728

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 728

Met	Leu	Pro	Val	Asn	Gln	Thr	Tyr	Ala	Gln	Phe	Ser	Asp	Thr	Ala	Phe
1				5					10					15	

Val	Ser	Ala	Tyr	Ile	Ile	Tyr	Val	Leu	Ala	Leu	Ile	Leu	Ser	Leu	Val
			20					25					30		

Tyr	Tyr	Val	Lys	Gln	Gln	Gly	Ile	Ile	Asp	Ala	Arg	Arg	Glu	Gln	Thr
		35					40					45			

Arg	Val	Ser	Glu	Leu	Val	Gly	Ala	Gly	Gly	Ser	Ala	Asp	Val	Asp	Thr
	50					55					60				

Asp	Leu	Pro	Asp	Asp	Ile	Ala	Asp	Gly	Val	Leu	Ala	Asp	Glu	Asp	Leu
	65				70					75					80

Ala	Lys	Arg	Glu	Glu	Thr	Ala	Arg	Lys	Leu	Ala	Asn	Met	Thr	Gln	Ser
				85					90					95	

Leu	Met	Trp	Leu	Gly	Val	Met	Val	His	Leu	Val	Ser	Val	Val	Met	Arg
			100					105						110	

Ala	Leu	Ser	Ala	Ser	Arg	Phe	Pro	Phe	Gly	Asn	Leu	Tyr	Glu	Tyr	Ile
			115				120					125			

Leu	Met	Val	Thr	Leu	Phe	Ala	Met	Ile	Gly	Ala	Val	Leu	Ile	Leu	Gln
			130			135					140				

Arg	Pro	Gln	Phe	Arg	Val	Val	Trp	Pro	Trp	Ile	Leu	Thr	Pro	Met	Leu
145					150					155					160

Ala Leu Leu Phe Tyr Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro  
 165 170 175

Val Val Pro Ala Leu Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser  
 180 185 190

Val Ser Ile Gly Ala Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu  
 195 200 205

Leu Tyr Ile Leu Arg Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe  
 210 215 220

Phe Gly Ala Val Ala Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn  
 225 230 235 240

Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly  
 245 250 255

Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp  
 260 265 270

Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr  
 275 280 285

Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn  
 290 295 300

Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu  
 305 310 315 320

Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu  
 325 330 335

Asn

<210> 729  
 <211> 326  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(303)  
 <223> FRXA00388

<400> 729  
 acc ctg gat aac ctg gca tac aag acc gcg atc tgg act gtc cca atc 48  
 Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile  
 1 5 10 15

ttc ggc ctg ggc atc atc ttg ggt gcc atc tgg gca gaa gca gcc tgg 96  
 Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp  
 20 25 30

ggt cgt ttc tgg gga tgg gat cct aag gaa aca gtc tcc ttc atc acc 144  
 Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr  
 35 40 45

tgg gtt ctc tac gct ggt tac ctc cac gca cgt gca act gct ggt tgg 192

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp  
 50 55 60

cgc aac acc aac gct gca tgg atc aac atc ctg gcg ctg gtc acg atg 240  
 Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met  
 65 70 75 80

att ttt aat ctg ttc ttc atc aac atg gtc gta tct ggt ctg cac tct 288  
 Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser  
 85 90 95

tac gcc gga ctg aac taagcacttt tgggtggcgg ggt 326  
 Tyr Ala Gly Leu Asn  
 100

<210> 730  
 <211> 101  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 730  
 Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile  
 1 5 10 15

Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp  
 20 25 30

Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr  
 35 40 45

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp  
 50 55 60

Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met  
 65 70 75 80

Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser  
 85 90 95

Tyr Ala Gly Leu Asn  
 100

<210> 731  
 <211> 610  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(610)  
 <223> FRXA00386

<400> 731  
 gaagagtact tcgaccacga cgactaacac cgcaatttaa aggcttttca agcctgcccc 60

acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac 115  
 Met Leu Pro Val Asn  
 1 5

caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc 163  
 Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile  
                   10                                  15                                  20

atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa 211  
 Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln  
                   25                                  30                                  35

caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc 259  
 Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu  
                   40                                  45                                  50

gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac 307  
 Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp  
                   55                                  60                                  65

atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa 355  
 Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu  
                   70                                  75                                  80                                  85

acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc 403  
 Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly  
                   90                                  95                                  100

gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc 451  
 Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser  
                   105                                  110                                  115

cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc 499  
 Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu  
                   120                                  125                                  130

ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc 547  
 Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg  
                   135                                  140                                  145

gtg gta tgg cca tgg atc ctc acc cca atg gct ggc act tgg ttt tct 595  
 Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala Gly Thr Trp Phe Ser  
                   150                                  155                                  160                                  165

acg gtg gca ccc agc 610  
 Thr Val Ala Pro Ser  
                   170

&lt;210&gt; 732

&lt;211&gt; 170

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 732

Met Leu Pro Val Asn Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe  
   1                                  5                                  10                                  15

Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val  
                   20                                  25                                  30

Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr  
                   35                                  40                                  45

Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr



50	55	60
Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu		
65	70	75 80
Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser		
	85	90 95
Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg		
	100	105 110
Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile		
	115	120 125
Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln		
	130	135 140
Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala		
	145	150 155 160
Gly Thr Trp Phe Ser Thr Val Ala Pro Ser		
	165	170

<210> 733  
 <211> 1095  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1072)  
 <223> RXA00945

<400> 733  
 tcacagtacc acccacaagc cacaaggagg gtatggaggt. gggcgtctaa agccaaattt 60

ttcccgggtgt ttgaggcgat tgcaccgtac actaatgtgc atg ctt gaa cgc ctc 115  
 Met Leu Glu Arg Leu 5  
 1

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg 163  
 Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val 20  
 10 15

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc 211  
 Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val 35  
 25 30

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc 259  
 Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg 50  
 40 45

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac 307  
 Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His 65  
 55 60

ctg act att ttg gcg atc act ttc gga ata ttc cca ctt atc ggc att 355  
 Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe Pro Leu Ile Gly Ile 85  
 70 75 80

ggg ctc gag ccg atg act gca ttt gtg tcg gaa gat att tat cgg gga	403
Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly	
90 95 100	
att ttg ttc ctc acg ctc gtt ccg tcc acc gtg cag tca tcg gtg gcg	451
Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala	
105 110 115	
ttt acc tcg atc gct aaa ggc aac gta gct ggt gcg att gtg tcg gca	499
Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala	
120 125 130	
tcg ctc tcc aac ctt gcg ggt gtt ttc ctc act ccg ctg ctg gtc atg	547
Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met	
135 140 145	
ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc	595
Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe	
150 155 160 165	
ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta	643
Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val	
170 175 180	
tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc	691
Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile	
185 190 195	
gtg gac cgc ggc tcg atc gcg atg gtc gtg tac tcc gcg ttt tct gcc	739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala	
200 205 210	
ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc	787
Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile	
215 220 225	
tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc	835
Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe	
230 235 240 245	
acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc	883
Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile	
250 255 260	
gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca	931
Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro	
265 270 275	
atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg	979
Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu	
280 285 290	
ccg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt	1027
Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu	
295 300 305	
gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc	1072
Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala	
310 315 320	
taaaagtcct cagtagctag cca	1095

&lt;210&gt; 734

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 734

```

Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val
 1           5           10           15

Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
      20           25           30

Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
 35           40           45

Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
 50           55           60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
 65           70           75           80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
      85           90           95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
      100           105           110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
      115           120           125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
      130           135           140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val
      145           150           155           160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
      165           170           175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
      180           185           190

Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
      195           200           205

Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
      210           215           220

Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
      225           230           235           240

Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
      245           250           255

Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu
      260           265           270

Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
      275           280           285

```

Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met  
290 295 300

Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln  
305                         310                         315                         320

Lys Ala Asn Ala

<210> 735

<211> 1281

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (1258)

<223> RXN02556

<400> 735

tgccatcata ttaaggccaa attgcttgga tcctgggatt tatttaatta gattaaatcc 60

gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115  
Leu Ile Val Ser Thr  
1 5

cag ccc att act gat cgc agc gca .ctc tcg gca gaa cac gca gag gtg 163  
Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val  
10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211  
Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr  
25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259  
Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala  
40 45 50

aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307  
Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala  
55 60 65

ctg	gcg	gct	tcg	att	gca	acg	ttt	gcc	acc	atg	ctc	ggt	act	cct	gat	355
Leu	Ala	Ala	Ser	Ile	Ala	Thr	Phe	Ala	Thr	Met	Leu	Val	Thr	Pro	Asp	
70					75					80					85	

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403  
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val  
90 95 100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451  
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu  
105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499  
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro  
120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547

Val	Ala	Glu	Ala	Trp	Asp	Ala	Val	Tyr	Trp	Ile	Met	Ala	Asn	Val	Leu		
135						140					145						
atc	ggt	ttt	gag	aac	aac	ctt	tat	gct	tcc	aac	gat	ctg	gag	cct	ggc	595	
Ile	Gly	Phe	Glu	Asn	Asn	Leu	Tyr	Ala	Ser	Asn	Asp	Leu	Glu	Pro	Gly		
150					155					160					165		
gac	gtc	ttc	cgc	gaa	gtc	acc	gtg	acc	gcg	aag	aag	cag	ctc	agc	gca	643	
Asp	Val	Phe	Arg	Glu	Val	Thr	Val	Thr	Ala	Lys	Lys	Gln	Leu	Ser	Ala		
				170					175					180			
acc	gtc	tgg	gaa	tac	acc	ctg	gca	ggt	gag	ctg	gtt	gcc	cca	gag	cca	691	
Thr	Val	Trp	Glu	Tyr	Thr	Leu	Ala	Gly	Glu	Leu	Val	Ala	Pro	Glu	Pro		
			185					190					195				
ggt	cag	tac	acc	tcc	atc	gga	gta	gtg	ctt	gac	gac	ggc	gcc	cgc	cag	739	
Gly	Gln	Tyr	Thr	Ser	Ile	Gly	Val	Val	Leu	Asp	Asp	Gly	Ala	Arg	Gln		
		200				205						210					
ctg	cgc	cag	tac	agc	ttg	ctc	ggc	ggc	tcc	gac	acc	gag	tac	cgc	att	787	
Leu	Arg	Gln	Tyr	Ser	Leu	Leu	Gly	Gly	Ser	Asp	Thr	Glu	Tyr	Arg	Ile		
		215				220					225						
gcg	gtt	gag	gat	aac	ggc	gag	gtt	tct	gga	ttc	ctg	cgt	gat	cgc	gta	835	
Ala	Val	Glu	Asp	Asn	Gly	Glu	Val	Ser	Gly	Phe	Leu	Arg	Asp	Arg	Val		
230					235					240					245		
tcc	gtt	ggt	gac	aag	att	gaa	gcc	acc	atc	gcg	gcc	ggc	gac	ctg	gtt	883	
Ser	Val	Gly	Asp	Lys	Ile	Glu	Ala	Thr	Ile	Ala	Ala	Gly	Asp	Leu	Val		
				250					255					260			
ctt	aac	aag	gac	acc	aat	cca	gtt	gtg	ctg	att	tcc	cag	ggc	atc	ggc	931	
Leu	Asn	Lys	Asp	Thr	Asn	Pro	Val	Val	Leu	Ile	Ser	Gln	Gly	Ile	Gly		
			265				270						275				
tcc	acc	cca	atg	gtg	ggc	atg	ctc	gca	ggt	atg	aac	cct	gaa	cgt	gac	979	
Ser	Thr	Pro	Met	Val	Gly	Met	Leu	Ala	Gly	Met	Asn	Pro	Glu	Arg	Asp		
		280					285					290					
gtt	gtg	gtt	ttg	cat	gct	gac	cag	gcc	gag	tcc	acc	tac	gcg	cag	gtg	1027	
Val	Val	Val	Leu	His	Ala	Asp	Gln	Ala	Glu	Ser	Thr	Tyr	Ala	Gln	Val		
		295				300					305						
gag	gaa	gtg	cag	ggg	ctc	gtc	gaa	aag	ctc	cct	aag	gct	gcg	ttt	gaa	1075	
Glu	Glu	Val	Gln	Gly	Leu	Val	Glu	Lys	Leu	Pro	Lys	Ala	Ala	Phe	Glu		
310					315					320					325		
atc	ttc	tac	cgc	gac	aac	gac	cag	tgg	ctc	gag	gtc	gct	ggc	cgc	att	1123	
Ile	Phe	Tyr	Arg	Asp	Asn	Asp	Gln	Trp	Leu	Glu	Val	Ala	Gly	Arg	Ile		
				330					335					340			
cca	tca	ggt	gcg	tcc	gtg	tac	ctg	tgc	ggt	ggc	gtg	gaa	ttc	ttg	aag	1171	
Pro	Ser	Gly	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Gly	Val	Glu	Phe	Leu	Lys		
			345					350					355				
aac	gtg	cgt	gag	cag	atc	gag	gcg	ctc	gat	gag	cag	cct	cgc	gac	gta	1219	
Asn	Val	Arg	Glu	Gln	Ile	Glu	Ala	Leu	Asp	Glu	Gln	Pro	Arg	Asp	Val		
		360					365					370					
aac	ttc	gag	ctc	ttc	gca	cca	aac	gac	tgg	ctg	att	tcc	taagcccaca			1268	
Asn	Phe	Glu	Leu	Phe	Ala	Pro	Asn	Asp	Trp	Leu	Ile	Ser					

375

380

385

ccccagaact tcc

1281

&lt;210&gt; 736

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 736

Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala  
 1 5 10 15

Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys  
 20 25 30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  
 35 40 45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly  
 50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met  
 65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  
 85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile  
 100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu  
 115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile  
 130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn  
 145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys  
 165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu  
 180 185 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp  
 195 200 205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp  
 210 215 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe  
 225 230 235 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala  
 245 250 255

Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile  
 260 265 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met  
 275 280 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser  
 290 295 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro  
 305 310 315 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu  
 325 330 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly  
 340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu  
 355 360 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu  
 370 375 380

Ile Ser  
 385

<210> 737  
 <211> 1281  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1258)  
 <223> FRXA02556

<400> 737  
 tgccatcata ttaaggccaa attgcttggg tctctgggatt tatttaatta gattaaatcc 60

gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115  
 Leu Ile Val Ser Thr  
 1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163  
 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val  
 10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211  
 Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr  
 25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259  
 Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala  
 40 45 50

aac acc ttc aac ggt ggc aat cag aag caa ggc gat cag cag aag gcg 307  
 Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala  
 55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355  
 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp

70	75	80	85	
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val	90	95	100	403
tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu	105	110	115	451
ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro	120	125	130	499
gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu	135	140	145	547
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly	150	155	160	595
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala	170	175	180	643
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro	185	190	195	691
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln	200	205	210	739
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile	215	220	225	787
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val	230	235	240	835
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val	250	255	260	883
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly	265	270	275	931
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp	280	285	290	979
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val	295	300	305	1027
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu	310	315	320	1075
			325	



atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att 1123  
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile  
                   330                  335                  340

cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag 1171  
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys  
                   345                  350                  355

aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta 1219  
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val  
                   360                  365                  370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268  
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser  
                   375                  380                  385

ccccagaact tcc 1281

<210> 738

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala  
   1                  5                  10                  15

Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys  
                   20                  25                  30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  
                   35                  40                  45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly  
                   50                  55                  60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met  
   65                  70                  75                  80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  
                   85                  90                  95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile  
                   100                  105                  110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu  
                   115                  120                  125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile  
                   130                  135                  140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn  
   145                  150                  155                  160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys  
                   165                  170                  175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu  
                   180                  185                  190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp  
 195 200 205  
 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp  
 210 215 220  
 Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe  
 225 230 235 240  
 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala  
 245 250 255  
 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile  
 260 265 270  
 Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met  
 275 280 285  
 Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser  
 290 295 300  
 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro  
 305 310 315 320  
 Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu  
 325 330 335  
 Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly  
 340 345 350  
 Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu  
 355 360 365  
 Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu  
 370 375 380  
 Ile Ser  
 385

<210> 739  
 <211> 1200  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1177)  
 <223> RXA01392

<400> 739  
 gtctgcaatc accccgaaca tttgttcaat cggtgatttt cattccactt cgtaatatg 60  
 ttgacatatc atctaaattt ccaagagagg acaccacaca gtg gct aac acg tca 115  
 Val Ala Asn Thr Ser  
 1 5  
 tcc gat tgg gca ggc gcc cca caa aat gca tca gca gac ggc gag ttc 163  
 Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser Ala Asp Gly Glu Phe  
 10 15 20

gtt cgc gat acc aac tac atc gat gac cgc atc gtc gca gac gtt cca	211
Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile Val Ala Asp Val Pro	
25 30 35	
gcg gga tcc gaa cca att gct cag gaa gat ggc act ttc cat tgg cct	259
Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly Thr Phe His Trp Pro	
40 45 50	
gtc gag gct ggt cgc tac cgt tta gtc gct gcc cgc gca tgt cca tgg	307
Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala Arg Ala Cys Pro Trp	
55 60 65	
gca cac cgc act gtt atc acc cgt cgt ctt ctc ggc ctg gag aac gtg	355
Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu Gly Leu Glu Asn Val	
70 75 80 85	
atc tcg ctt ggt ctg acc ggc ccg act cac gac gtt cgt tcc tgg act	403
Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp Val Arg Ser Trp Thr	
90 95 100	
ttc gat tta gat cca aac cat ctt gat ccc gtg ctg cag att cct cgt	451
Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val Leu Gln Ile Pro Arg	
105 110 115	
cta cag gac gcg tat ttc aac cgc ttc ccc gat tac ccg cgc ggc att	499
Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp Tyr Pro Arg Gly Ile	
120 125 130	
act gtc cca gcg ctc gtg gag gaa tcg tct aag aag gtc gtc acc aac	547
Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys Lys Val Val Thr Asn	
135 140 145	
gat tac cct tcc atc acc atc gat ttc aat ctt gag tgg aag cag ttc	595
Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu Glu Trp Lys Gln Phe	
150 155 160 165	
cac cgt gag ggt gcg cct aac ctc tac ccc gcg gag ctg cgc gag gag	643
His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala Glu Leu Arg Glu Glu	
170 175 180	
atg gcg ccg gtg atg aag cgc atc ttc act gag gtc aac aac ggc gta	691
Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu Val Asn Asn Gly Val	
185 190 195	
tac agg acc ggc ttt gcc ggt agc cag gaa gcg cac aac gag gcg tac	739
Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr	
200 205 210	
aag cgg ctt tgg gtt gcg ttg gac tgg cta gaa gat cgc tta tcg acg	787
Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu Asp Arg Leu Ser Thr	
215 220 225	
cga cgt tac ctc atg ggg gat cac atc acc gag gcg gat atc cgc ctc	835
Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu	
230 235 240 245	
tac cca acc ctc gtg cgt ttc gat gcc gtc tac cac gga cac ttc aag	883
Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr His Gly His Phe Lys	
250 255 260	

tgt ggc cgc aac aag atc acc gaa atg ccg aat cta tgg ggc tac ctg 931  
 Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn Leu Trp Gly Tyr Leu  
                   265                                  270                                  275  
  
 cgg gat ctt ttc cag acc cca ggc ttt ggc gac acc acc gat ttc acc 979  
 Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp Thr Thr Asp Phe Thr  
                   280                                  285                                  290  
  
 gaa atc aag cag cac tac tac atc acc cac gcg gag att aac ccc acc 1027  
 Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala Glu Ile Asn Pro Thr  
                   295                                  300                                  305  
  
 cgg atc gtt cca gtc gga cca gat ctg tct ggt ttc gcg aca cca cac 1075  
 Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly Phe Ala Thr Pro His  
 310                                  315                                  320                                  325  
  
 ggc cgt gaa aag ctc ggc gga tcc cca ttt gct gaa ggt gtt act ctg 1123  
 Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala Glu Gly Val Thr Leu  
                                   330                                  335                                  340  
  
 cct ggc cca att cct gcg ggc gaa gaa gtg aaa aac cct gaa cct ttt 1171  
 Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys Asn Pro Glu Pro Phe  
                                   345                                  350                                  355  
  
 cag aag taactaaggc cgcaatccct cga 1200  
 Gln Lys

<210> 740  
 <211> 359  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 740  
 Val Ala Asn Thr Ser Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser  
   1                                  5                                  10                                  15  
  
 Ala Asp Gly Glu Phe Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile  
                   20                                  25                                  30  
  
 Val Ala Asp Val Pro Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly  
                   35                                  40                                  45  
  
 Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala  
                   50                                  55                                  60  
  
 Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu  
                   65                                  70                                  75                                  80  
  
 Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp  
                                   85                                  90                                  95  
  
 Val Arg Ser Trp Thr Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val  
                   100                                  105                                  110  
  
 Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp  
                   115                                  120                                  125  
  
 Tyr Pro Arg Gly Ile Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys  
                   130                                  135                                  140

Lys Val Val Thr Asn Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu  
145 150 155 160

Glu Trp Lys Gln Phe His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala  
165 170 175

Glu Leu Arg Glu Glu Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu  
180 185 190

Val Asn Asn Gly Val Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala  
195 200 205

His Asn Glu Ala Tyr Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu  
210 215 220

Asp Arg Leu Ser Thr Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu  
225 230 235 240

Ala Asp Ile Arg Leu Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr  
245 250 255

His Gly His Phe Lys Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn  
260 265 270

Leu Trp Gly Tyr Leu Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp  
275 280 285

Thr Thr Asp Phe Thr Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala  
290 295 300

Glu Ile Asn Pro Thr Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly  
305 310 315 320

Phe Ala Thr Pro His Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala  
325 330 335

Glu Gly Val Thr Leu Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys  
340 345 350

Asn Pro Glu Pro Phe Gln Lys  
355

<210> 741

<211> 1227

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1204)

<223> RXA00800

<400> 741

gactccgcag ggatggccta caagtacggt cacggactta atttctagat tgtaggtagt 60

ctcgtgggca caactgaaat cttattgaaa aggagtgtcc atg agc act gta gtg 115  
Met Ser Thr Val Val  
1 5

cct gga att gtc gca ctg tcc aag ggt gca ccg gta gaa aaa gta aac	163
Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro Val Glu Lys Val Asn	
10 15 20	
gtt gtt gtc cct gat cca ggt gct aac gat gtc atc gtc aag att cag	211
Val Val Val Pro Asp Pro Gly Ala Asn Asp Val Ile Val Lys Ile Gln	
25 30 35	
gcc tgc ggt gtg tgc cac acc gac ttg gcc tac cgc gat ggc gat att	259
Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr Arg Asp Gly Asp Ile	
40 45 50	
tca gat gag ttc cct tac ctg ctg ggc cac gag gca gca ggc att gtt	307
Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu Ala Ala Gly Ile Val	
55 60 65	
gag gag gta ggc gag tcc gtc acc cac gtt gag gtc ggc gat ttc gtc	355
Glu Glu Val Gly Glu Ser Val Thr His Val Glu Val Gly Asp Phe Val	
70 75 80 85	
atc ttg aac tgg cgt gca gtg tgc ggc gag tgc cgt gca tgt aag aag	403
Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys Arg Ala Cys Lys Lys	
90 95 100	
ggc gag cca aag tac tgc ttt aac acc cac aac gcc tct aag aag atg	451
Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn Ala Ser Lys Lys Met	
105 110 115	
acc ctg gaa gac ggc acc gag ctg tcc cca gca ctg ggt att ggc gcg	499
Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala Leu Gly Ile Gly Ala	
120 125 130	
ttc ttg gaa aag acc ctg gtc cac gaa ggc cag tgc acc aag gtt aac	547
Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln Cys Thr Lys Val Asn	
135 140 145	
cct gag gaa gat cca gca gca gct ggc ctt ctg ggt tgt ggc atc atg	595
Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu Gly Cys Gly Ile Met	
150 155 160 165	
gca ggc ctt ggc gct gcg gtg aac acc ggt gat att aag cgt ggc gag	643
Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp Ile Lys Arg Gly Glu	
170 175 180	
tcc gta gca gtc ttc ggc ctt ggt ggc gtg ggc atg gca gct att gct	691
Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly Met Ala Ala Ile Ala	
185 190 195	
ggc gcc aag att gct ggc gct tcc aag atc att gct gtt gat atc gat	739
Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile Ala Val Asp Ile Asp	
200 205 210	
gag aag aag ctg gag tgg gcg aag gaa ttc ggc gca acc cac acc att	787
Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly Ala Thr His Thr Ile	
215 220 225	
aat tcc tct ggt ctt ggt ggc gaa ggt gat gcc tct gag gtc gtg gca	835
Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala Ser Glu Val Val Ala	
230 235 240 245	
aag gtt cgt gag ctg acc gat ggt ttc ggc acc gat gtc tcc atc gat	883

Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr Asp Val Ser Ile Asp  
 250 255 260

gcg gta ggc atc atg ccg acc tgg cag cag gcg ttt tac tcc cgt gac 931  
 Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala Phe Tyr Ser Arg Asp  
 265 270 275

cat gca ggc cgc atg gtg atg gtg ggc gtt cca aac ctg acg tct cgc 979  
 His Ala Gly Arg Met Val Met Val Gly Val Pro Asn Leu Thr Ser Arg  
 280 285 290

gta gat gtt cct gcg att gat ttt tac ggt cgc ggt gga tcc gtg cgc 1027  
 Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg Gly Gly Ser Val Arg  
 295 300 305

cct gca tgg tac ggc gac tgc ctg cct gag cgt gat ttc cca act tat 1075  
 Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg Asp Phe Pro Thr Tyr  
 310 315 320 325

gtg gat ctg cac ctg cag ggt cgt ttc cca ctg gat aag ttt gtt tct 1123  
 Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu Asp Lys Phe Val Ser  
 330 335 340

gag cgt att ggt ctt gat gat gtt gaa gag gct ttc aac acc atg aag 1171  
 Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala Phe Asn Thr Met Lys  
 345 350 355

gct ggc gac gtg ctg cgt tct gtg gtg gag atc taaatggctc acgacggatt 1224  
 Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile  
 360 365

gcg 1227

<210> 742

<211> 368

<212> PRT

<213> Corynebacterium glutamicum

<400> 742

Met Ser Thr Val Val Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro  
 1 5 10 15

Val Glu Lys Val Asn Val Val Val Pro Asp Pro Gly Ala Asn Asp Val  
 20 25 30

Ile Val Lys Ile Gln Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr  
 35 40 45

Arg Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu  
 50 55 60

Ala Ala Gly Ile Val Glu Glu Val Gly Glu Ser Val Thr His Val Glu  
 65 70 75 80

Val Gly Asp Phe Val Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys  
 85 90 95

Arg Ala Cys Lys Lys Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn  
 100 105 110

Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala  
 115 120 125  
 Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln  
 130 135 140  
 Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu  
 145 150 155 160  
 Gly Cys Gly Ile Met Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp  
 165 170 175  
 Ile Lys Arg Gly Glu Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly  
 180 185 190  
 Met Ala Ala Ile Ala Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile  
 195 200 205  
 Ala Val Asp Ile Asp Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly  
 210 215 220  
 Ala Thr His Thr Ile Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala  
 225 230 235 240  
 Ser Glu Val Val Ala Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr  
 245 250 255  
 Asp Val Ser Ile Asp Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala  
 260 265 270  
 Phe Tyr Ser Arg Asp His Ala Gly Arg Met Val Met Val Gly Val Pro  
 275 280 285  
 Asn Leu Thr Ser Arg Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg  
 290 295 300  
 Gly Gly Ser Val Arg Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg  
 305 310 315 320  
 Asp Phe Pro Thr Tyr Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu  
 325 330 335  
 Asp Lys Phe Val Ser Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala  
 340 345 350  
 Phe Asn Thr Met Lys Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile  
 355 360 365

&lt;210&gt; 743

&lt;211&gt; 1011

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(988)

&lt;223&gt; RXA02143



&lt;400&gt; 743

tcttcacac tatttacttc attcagtagg cagtaaggaa tcctcaacgt tgttgaggtt 60

ccctatgccc ttcacttcca cagtcgagat tcaaagggaa atg atg gaa acc aac 115  
 Met Met Glu Thr Asn  
 1 5

ccg cag acc cca gag gga aat agc atg gct aaa ccc tct gct aag aag 163  
 Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys Pro Ser Ala Lys Lys  
 10 15 20

gtc aag aat cgc cgc aag gtc cgg cgc acc gtc gca ggt gca ttg gct 211  
 Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val Ala Gly Ala Leu Ala  
 25 30 35

ctg acc att gga ctg agc gga gca gga atc ctc gca acc gcg atc act 259  
 Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu Ala Thr Ala Ile Thr  
 40 45 50

cca gat gct caa gtt gct acc gct cag cgt gac gat cag gca ctt atc 307  
 Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp Asp Gln Ala Leu Ile  
 55 60 65

tcc gag ggt aaa gac ctc tac gat gtc gcc tgc atc acc tgc cac ggc 355  
 Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys Ile Thr Cys His Gly  
 70 75 80 85

gta aac ctc caa ggt gtt gag gac cgc ggt cct tcc ctc gta ggt gtt 403  
 Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro Ser Leu Val Gly Val  
 90 95 100

ggc gaa ggc gca gtg tac ttc caa gtt cac tcc ggc cgt atg cca ata 451  
 Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser Gly Arg Met Pro Ile  
 105 110 115

ctg cgt aac gag gct cag gct gag cgc aag gct cct cgt tac acc gag 499  
 Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala Pro Arg Tyr Thr Glu  
 120 125 130

gca cag acc ctt gcg atc gct gca tat gtt gca gct aat ggc ggt ggc 547  
 Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala Ala Asn Gly Gly Gly  
 135 140 145

cca gga ctc gtt tac aac gag gac ggc acc ctc gcc atg gag gag ctc 595  
 Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu Ala Met Glu Glu Leu  
 150 155 160 165

cgt ggc gaa aac tac gac gga cag att acc tcc gcc gac gtc gct cgc 643  
 Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser Ala Asp Val Ala Arg  
 170 175 180

ggc gga gat ctg ttc cgc ctg aac tgt gca tcc tgc cac aac ttc act 691  
 Gly Gly Asp Leu Phe Arg Leu Asn Cys Ala Ser Cys His Asn Phe Thr  
 185 190 195

ggc gga gat ctg ttc cgc ctg aac tgt gca tcc tgc cac aac ttc act 739  
 Gly Arg Gly Gly Ala Leu Ser Ser Gly Lys Tyr Ala Pro Asn Leu Asp  
 200 205 210

gct gca aac gag cag gaa atc tac cag gct atg ctt acc ggt cct cag 787

Ala Ala Asn Glu Gln Glu Ile Tyr Gln Ala Met Leu Thr Gly Pro Gln  
 215 220 225

aac atg cct aag ttc tcc gat cgt cag ctc tcc gca gat gag aag aag 835  
 Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser Ala Asp Glu Lys Lys  
 230 235 240 245

gac atc atc gcc ttc atc aag tcc acc aag gag act cca tca cct ggt 883  
 Asp Ile Ile Ala Phe Ile Lys Ser Thr Lys Glu Thr Pro Ser Pro Gly  
 250 255 260

ggt tac tca ctc ggt agc ttg ggc cca gtg gct gag ggt ctg ttc atg 931  
 Gly Tyr Ser Leu Gly Ser Leu Gly Pro Val Ala Glu Gly Leu Phe Met  
 265 270 275

tgg gta ttc ggc atc ttg gtc ctc gtg gcc gcc gct atg tgg att gga 979  
 Trp Val Phe Gly Ile Leu Val Leu Val Ala Ala Ala Met Trp Ile Gly  
 280 285 290

tca cgt tca tgagtaacaa caacgacaaa cag 1011  
 Ser Arg Ser  
 295

<210> 744  
 <211> 296  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 744  
 Met Met Glu Thr Asn Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys  
 1 5 10 15

Pro Ser Ala Lys Lys Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val  
 20 25 30

Ala Gly Ala Leu Ala Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu  
 35 40 45

Ala Thr Ala Ile Thr Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp  
 50 55 60

Asp Gln Ala Leu Ile Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys  
 65 70 75 80

Ile Thr Cys His Gly Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro  
 85 90 95

Ser Leu Val Gly Val Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser  
 100 105 110

Gly Arg Met Pro Ile Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala  
 115 120 125

Pro Arg Tyr Thr Glu Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala  
 130 135 140

Ala Asn Gly Gly Gly Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu  
 145 150 155 160

Ala Met Glu Glu Leu Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser

	165		170		175
Ala Asp Val	Ala Arg Gly Gly Asp	Leu Phe Arg Leu Asn Cys	Ala Ser		
	180	185	190		
Cys His Asn	Phe Thr Gly Arg Gly Gly	Ala Leu Ser Ser	Gly Lys Tyr		
	195	200	205		
Ala Pro Asn	Leu Asp Ala Ala Asn Glu Gln Glu	Ile Tyr Gln Ala Met			
	210	215	220		
Leu Thr Gly	Pro Gln Asn Met Pro Lys Phe	Ser Asp Arg Gln Leu Ser			
	225	230	235	240	
Ala Asp Glu	Lys Lys Asp Ile Ile Ala Phe	Ile Lys Ser Thr Lys Glu			
	245	250	255		
Thr Pro Ser	Pro Gly Gly Tyr Ser Leu Gly	Ser Leu Gly Pro Val Ala			
	260	265	270		
Glu Gly Leu	Phe Met Trp Val Phe Gly	Ile Leu Val Leu Val Ala Ala			
	275	280	285		
Ala Met Trp	Ile Gly Ser Arg Ser				
	290	295			

<210> 745  
 <211> 502  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(502)  
 <223> RXN03096

<400> 745  
 aagatcatgc tcatcgaagc cggcgcccgga agatggcagt tggctggcat gggtccttat 60

cgcaggcgcc gttgtcacct cactgctcac cttgtacacc atg gtt ctg gtc tgg 115  
 Met Val Leu Val Trp  
 1 5

tcc aag gcc ttc tgg cgc gac cgt aaa gac gcc ccc gat gga gca acc 163  
 Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala Pro Asp Gly Ala Thr  
 10 15 20

gca cta gca aga ccc gca cct ttg gta gat atc caa gac gaa gtc gcc 211  
 Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile Gln Asp Glu Val Ala  
 25 30 35

gtt aaa gac cgc aac gat gtc gga cgg atg cct tgg ggc atg gtc ttc 259  
 Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro Trp Gly Met Val Phe  
 40 45 50

tcc act gcc ctg ttg gtt tcc gca tcc ctt gct gta tcc gtg ctc gca 307  
 Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala Val Ser Val Leu Ala  
 55 60 65

gga cca ctg tca tct att act gga cgc gcc gcc gaa tcc gca caa gat 355

Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala Glu Ser Ala Gln Asp  
 70 75 80 85  
 gtc aac atc tac cgc gcc gca gta ctc ggc cca act acc tcg acc cat 403  
 Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro Thr Thr Ser Thr His  
 90 95 100  
 cac gca cac tcg aga tgg agc gtt acg acg cca acc gcg atg aca tca 451  
 His Ala His Ser Arg Trp Ser Val Thr Thr Pro Thr Ala Met Thr Ser  
 105 110 115  
 acc acc gcg tcg aca cca atg gaa cgg agg acc aac cat gat cag tgg 499  
 Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr Asn His Asp Gln Trp  
 120 125 130  
 att 502  
 Ile

<210> 746  
 <211> 134  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 746  
 Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala  
 1 5 10 15  
 Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile  
 20 25 30  
 Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro  
 35 40 45  
 Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala  
 50 55 60  
 Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala  
 65 70 75 80  
 Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro  
 85 90 95  
 Thr Thr Ser Thr His His Ala His Ser Arg Trp Ser Val Thr Thr Pro  
 100 105 110  
 Thr Ala Met Thr Ser Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr  
 115 120 125  
 Asn His Asp Gln Trp Ile  
 130

<210> 747  
 <211> 504  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS

&lt;222&gt; (101)..(481)

&lt;223&gt; RXN02036

&lt;400&gt; 747

ctaaaatgga aggcaatgga tacccgccgc atgaacctcc gccaatggaa aatcctcggt 60

gccctcatct ctgctgcagt ggcggctctc ggagggtggt gtg cat att cct ttt 115  
 Val His Ile Pro Phe  
 1 5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163  
 Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys  
 10 15 20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211  
 Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser  
 25 30 35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259  
 Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala  
 40 45 50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307  
 Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val  
 55 60 65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355  
 Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe  
 70 75 80 85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403  
 Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe  
 90 95 100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451  
 Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys  
 105 110 115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501  
 Val Arg Glu Arg Ala Ala Gly Leu Ser Asn  
 120 125

ttt 504

&lt;210&gt; 748

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 748

Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys  
 1 5 10 15

Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro  
 20 25 30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala  
 35 40 45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala

50					55					60					
Phe	Arg	Ser	Gly	Val	Gln	Ala	Ala	Ile	Ala	Asp	Gly	Tyr	Thr	Ser	Ala
65					70					75					80
Thr	Ser	Val	Gly	Phe	Glu	Met	Thr	Val	Ser	Leu	Ile	Leu	Phe	Ile	Ile
				85					90					95	
Ala	Gly	Leu	Cys	Phe	Leu	Gly	Trp	Ile	Pro	Met	Phe	Ile	Asn	Asn	Arg
			100					105					110		
Gln	Val	Ala	Arg	Lys	Val	Arg	Glu	Arg	Ala	Ala	Gly	Leu	Ser	Asn	
		115					120					125			

<210> 749  
<211> 882  
<212> DNA  
<213> Corynebacterium glutamicum

```
<220>  
<221> CDS  
<222> (101)..(859)  
<223> RXN02765
```

[illegible]

Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala Trp Glu Glu Gln Pro  
 120 125 130  
 ggt cga atc ggt gaa ttg ttg gag ccg att aat cgc gtg aac cag gtt 547  
 Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val  
 135 140 145  
 ggt cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca 595  
 Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro  
 150 155 160 165  
 cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act 643  
 Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr  
 170 175 180  
 gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag 691  
 Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu  
 185 190 195  
 gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt 739  
 Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val  
 200 205 210  
 ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac 787  
 Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn  
 215 220 225  
 aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc 835  
 Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu  
 230 235 240 245  
 gtg tcg tat gtt tct gac aag att tgaggtatgt cggaatacaa acc 882  
 Val Ser Tyr Val Ser Asp Lys Ile  
 250

&lt;210&gt; 750

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 750

Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly  
 1 5 10 15  
 Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg  
 20 25 30  
 Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly  
 35 40 45  
 Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val  
 50 55 60  
 Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp  
 65 70 75 80  
 Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu  
 85 90 95  
 Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His

100	105	110
Ala Pro Glu Pro Val Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala 115 120 125		
Trp Glu Glu Gln Pro Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn 130 135 140		
Arg Val Asn Gln Val Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr 145 150 155 160		
Ala Gly Thr Gln Pro Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg 165 170 175		
Pro His Gly Phe Thr Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu 180 185 190		
Gly Ala Val Asp Glu Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu 195 200 205		
Ile Glu Gln Leu Val Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln 210 215 220		
Glu Phe Ser Glu Asn Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg 225 230 235 240		
Val Glu Ser Thr Leu Val Ser Tyr Val Ser Asp Lys Ile 245 250		
<210> 751		
<211> 1059		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(1036)		
<223> RXN02206		
<400> 751		
ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccgtact 60		
accttatgac ctcagtagtg tgggtggcgt gaaacagcga atg gtc ggt tca agt 115		
	Met Val Gly Ser Ser	
	1 5	
ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163		
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser		
	10 15 20	
ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211		
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn		
	25 30 35	
tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259		
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val		
	40 45 50	
gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307		
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser		



55	60	65	
gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu 70 75 80 85			355
ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp 90 95 100			403
gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val 105 110 115			451
ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu 120 125 130			499
gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly 135 140 145			547
tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala 150 155 160 165			595
gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu 170 175 180			643
ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu 185 190 195			691
ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr 200 205 210			739
gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr 215 220 225			787
gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile 230 235 240 245			835
att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro 250 255 260			883
gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala 265 270 275			931
gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys 280 285 290			979
gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp 295 300 305			1027

gtc tcc ctg tgacttggtc caattacatt cac  
Val Ser Leu  
310

1059

<210> 752  
<211> 312  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 752  
Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr  
1 5 10 15  
Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe  
20 25 30  
Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn  
35 40 45  
Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala  
50 55 60  
Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn  
65 70 75 80  
Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu  
85 90 95  
Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu  
100 105 110  
Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu  
115 120 125  
Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr  
130 135 140  
Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala  
145 150 155 160  
Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln  
165 170 175  
Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro  
180 185 190  
Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly  
195 200 205  
Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser  
210 215 220  
Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp  
225 230 235 240  
Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly  
245 250 255  
Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg

260 265 270  
 Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu  
 275 280 285  
 Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr  
 290 295 300  
 Gln Ala Leu Asp Asp Val Ser Leu  
 305 310  
  
 <210> 753  
 <211> 747  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(724)  
 <223> RXN02554  
  
 <400> 753  
 gcttttgaag tgtgtcgcgt gtgcggactg aaatagtttc cgcttcaact tggttgctaa 60  
  
 ggataggctc cataaaaaata accaaaggcg gaaaatttca atg tca cac act aag 115  
 Met Ser His Thr Lys  
 1 5  
  
 cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163  
 Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala  
 10 15 20  
  
 agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt 211  
 Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly  
 25 30 35  
  
 gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg 259  
 Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala  
 40 45 50  
  
 gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc 307  
 Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe  
 55 60 65  
  
 ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355  
 Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu  
 70 75 80 85  
  
 gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403  
 Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn  
 90 95 100  
  
 ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att 451  
 Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile  
 105 110 115  
  
 att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac 499  
 Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His  
 120 125 130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att 547  
 Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile  
 135 140 145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595  
 Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu  
 150 155 160 165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643  
 Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn  
 170 175 180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691  
 Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn  
 185 190 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744  
 Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg  
 200 205

aac 747

<210> 754  
 <211> 208  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 754  
 Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val  
 1 5 10 15

Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys  
 20 25 30

Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile  
 35 40 45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp  
 50 55 60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val  
 65 70 75 80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His  
 85 90 95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg  
 100 105 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val  
 115 120 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly  
 130 135 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala  
 145 150 155 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile  
 165 170 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe  
 180 185 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg  
 195 200 205

<210> 755  
 <211> 933  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(910)  
 <223> RXN01204

<400> 755  
 ttacagcgag tttttcagac gtccatcgca ccgtgcacaa caacatttca ggtgcacggc 60

ccgaacacgg gagagaacgc tgagcggttac aacactgtcc atg aag ggc gaa ttc 115  
 Met Lys Gly Glu Phe  
 1 5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163  
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp  
 10 15 20

agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211  
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp  
 25 30 35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259  
 Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val  
 40 45 50

gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg 307  
 Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro  
 55 60 65

cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att 355  
 His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile  
 70 75 80 85

cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg 403  
 His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu  
 90 95 100

ccg atc ctg gcc acc atc ttc ttc gcg gct ctg ttg atg aac ctt gca 451  
 Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu Leu Met Asn Leu Ala  
 105 110 115

acg atc atc ccg gga cta aac atc tcc tcc aac tca cgt att gca ttc 499  
 Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn Ser Arg Ile Ala Phe  
 120 125 130

cca atc gtg atg gcg gta gct ggt tac atc gcg ttt atc tac gca ggc 547

Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala Phe Ile Tyr Ala Gly  
 135 140 145  
 tct aag cgt tac gga ttc ttc aaa tat gtg aag tct tct gtt gtg att 595  
 Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys Ser Ser Val Val Ile  
 150 155 160 165  
 ccg aac att cca cca gca ctt cac gtc ttg gtg gtt cca att gag ttc 643  
 Pro Asn Ile Pro Pro Ala Leu His Val Leu Val Val Pro Ile Glu Phe  
 170 175 180  
 ttc tct aca ttc atc ttg agg cca gtc acc ctg gca ctg cgt ttg atg 691  
 Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu Ala Leu Arg Leu Met  
 185 190 195  
 gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc tcc gca 739  
 Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Ser Ala  
 200 205 210  
 acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc 787  
 Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly  
 215 220 225  
 gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt 835  
 Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val  
 230 235 240 245  
 atc ttc ctg cag gca tac atc ttc gct ctg ctg gtc gct gta tac att 883  
 Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu Val Ala Val Tyr Ile  
 250 255 260  
 gag ctt tca ctt cac gcg gat tct cac tagatgaaaa aggtcgctat 930  
 Glu Leu Ser Leu His Ala Asp Ser His  
 265 270  
 taa 933  
  
 <210> 756  
 <211> 270  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 756  
 Met Lys Gly Glu Phe His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro  
 1 5 10 15  
 Gly His Val Thr Asp Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp  
 20 25 30  
 Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu  
 35 40 45  
 Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys  
 50 55 60  
 Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu  
 65 70 75 80  
 Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys  
 85 90 95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu  
 100 105 110  
 Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn  
 115 120 125  
 Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala  
 130 135 140  
 Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys  
 145 150 155 160  
 Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val  
 165 170 175  
 Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu  
 180 185 190  
 Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val  
 195 200 205  
 Leu Leu Phe Ser Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp  
 210 215 220  
 Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val  
 225 230 235 240  
 Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu  
 245 250 255  
 Val Ala Val Tyr Ile Glu Leu Ser Leu His Ala Asp Ser His  
 260 265 270

<210> 757  
 <211> 862  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(862)  
 <223> FRXA01204

<400> 757  
 ttacagcgag tttttcagac gtccatcgca ccgtgcacaa caacatttca ggtgcacggc 60  
 ccgaacacgg gagagaacgc tgagcggttac aacactgtcc atg aag ggc gaa ttc 115  
 Met Lys Gly Glu Phe  
 1 5  
 cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163  
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp  
 10 15 20  
 agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211  
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp  
 25 30 35  
 ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259

Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val  
           40                          45                          50  
 gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg 307  
 Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro  
           55                          60                          65  
 cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att 355  
 His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile  
           70                          75                          80                          85  
 cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg 403  
 His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu  
                           90                          95                          100  
 ccg atc ctg gcc acc atc ttc ttc gcg gct ctg ttg atg aac ctt gca 451  
 Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu Leu Met Asn Leu Ala  
                           105                          110                          115  
 acg atc atc ccg gga cta aac atc tcc tcc aac tca cgt att gca ttc 499  
 Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn Ser Arg Ile Ala Phe  
                           120                          125                          130  
 cca atc gtg atg gcg gta gct ggt tac atc gcg ttt atc tac gca ggc 547  
 Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala Phe Ile Tyr Ala Gly  
                           135                          140                          145  
 tct aag cgt tac gga ttc ttc aaa tat gtg aag tct tct gtt gtg att 595  
 Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys Ser Ser Val Val Ile  
                           150                          155                          160                          165  
 ccg aac att cca cca gca ctt cac gtc ttg gtg gtt cca att gag ttc 643  
 Pro Asn Ile Pro Pro Ala Leu His Val Leu Val Val Pro Ile Glu Phe  
                           170                          175                          180  
 ttc tct aca ttc atc ttg agg cca gtc acc ctg gca ctg cgt ttg atg 691  
 Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu Ala Leu Arg Leu Met  
                           185                          190                          195  
 gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc ttc gca 739  
 Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Phe Ala  
                           200                          205                          210  
 acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc 787  
 Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly  
                           215                          220                          225  
 gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt 835  
 Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val  
                           230                          235                          240                          245  
 atc ttc ctg cag gca tac atc ttc gct 862  
 Ile Phe Leu Gln Ala Tyr Ile Phe Ala  
                           250

&lt;210&gt; 758

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 758

```

Met Lys Gly Glu Phe His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro
 1           5           10           15

Gly His Val Thr Asp Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp
          20           25           30

Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
          35           40           45

Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
          50           55           60

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
          65           70           75           80

Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
          85           90           95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
          100           105           110

Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
          115           120           125

Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
          130           135           140

Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
          145           150           155           160

Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
          165           170           175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
          180           185           190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
          195           200           205

Leu Leu Phe Phe Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
          210           215           220

Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
          225           230           235           240

Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala
          245           250

```

&lt;210&gt; 759

&lt;211&gt; 1764

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1741)

&lt;223&gt; RXA01201

&lt;400&gt; 759

tcgggcaaac tcgagcgtct gcgggcaagc ttgcgataaa gacacgacga attagacaac 60

attagtaatg ctggaagaaa caaccgagag caggaagaac atg gcg gag ctg acg 115  
Met Ala Glu Leu Thr  
1 5

atc tcc tcc gat gag atc cgt agc gcg att gcg aac tac acc tcg agc 163  
Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala Asn Tyr Thr Ser Ser  
10 15 20

tac tcc gcg gag gcc tcc cgt gag gag gtc ggc gtg gtt att tcg gcc 211  
Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly Val Val Ile Ser Ala  
25 30 35

gct gac ggt atc gcc cag gtt tcg ggc ctc ccg tca gta atg gcg aat 259  
Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro Ser Val Met Ala Asn  
40 45 50

gag ctc ctc gaa ttc ccg ggc ggc gtc atc ggc gtc gca cag aac ctt 307  
Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly Val Ala Gln Asn Leu  
55 60 65

gaa gct gac cga gtc ggc gtc gtg gtc ctg ggt aac tac gag cta ctt 355  
Glu Ala Asp Arg Val Gly Val Val Val Leu Gly Asn Tyr Glu Leu Leu  
70 75 80 85

aaa gaa ggc gac caa gtt cgt cgt act gga gac gtt ctg tct atc cca 403  
Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp Val Leu Ser Ile Pro  
90 95 100

gtc ggc gag gca ttc ctt ggc cgc gtt atc aac ccc ctt ggc cag cca 451  
Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn Pro Leu Gly Gln Pro  
105 110 115

att gac ggc ctg ggc gaa att gca tcc gaa gag gac cgc gtc ctc gag 499  
Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu Asp Arg Val Leu Glu  
120 125 130

ctt cag gca cca acc gtg ctt gag cgc cag cct gtc gag gag cct ttg 547  
Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro Val Glu Glu Pro Leu  
135 140 145

gca acc ggc atc aag gct atc gat gca atg acc cca atc ggc cgc ggt 595  
Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr Pro Ile Gly Arg Gly  
150 155 160 165

cag cgt cag ctg atc att ggt gac cgt aag act ggc aag acc gca gtc 643  
Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr Gly Lys Thr Ala Val  
170 175 180

tgt gtc gat acc atc ctt aac cag aag gcc aac tgg gag acc ggc gac 691  
Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn Trp Glu Thr Gly Asp  
185 190 195

aag acc aag cag gtt cgc tgc atc tac gtc gca atc ggt cag aag ggc 739  
Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly  
200 205 210

tcc acc att gca gcc ctg cgt aag acc ctc gag gag cag ggc gct ctc 787  
Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu Glu Gln Gly Ala Leu  
215 220 225

gag tac acc acc atc gtg gct gca ccc gct tcc gat gct gca ggc ttc	835
Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser Asp Ala Ala Gly Phe	
230 235 240 245	
aag tgg ctt gca cca ttc gct ggc gct gct ctc gcc cag cac tgg atg	883
Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu Ala Gln His Trp Met	
250 255 260	
tac cag ggc aac cac gtc ctg gtc atc tac gat gat ctg acc aag cag	931
Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp Asp Leu Thr Lys Gln	
265 270 275	
gct gag gca tac cgt gct atc tcc ctg ctg ctg cgt cgc cca ccg ggc	979
Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly	
280 285 290	
cgc gaa gca tac cca ggt gac gtc ttc tac ctg cac tcc cgt ctg ctg	1027
Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu	
295 300 305	
gag cgc gct gcg aag ctg tcc gat gaa cta ggc gca ggt tct att aca	1075
Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly Ala Gly Ser Ile Thr	
310 315 320 325	
gca ctg cca atc att gag acc aag gct aat gac gtt tcc gcc ttc att	1123
Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp Val Ser Ala Phe Ile	
330 335 340	
cct acc aac gtg att tcc atc acc gac ggt cag gta ttc ctt gag tcc	1171
Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln Val Phe Leu Glu Ser	
345 350 355	
gac ctg ttc aac cgt ggc gtt cgc ccg gcg atc aac gtc ggt gta tcc	1219
Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile Asn Val Gly Val Ser	
360 365 370	
gtc tcc cgt gtc ggt ggc gca gct cag acc aag ggt atg aag aag gtt	1267
Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys Gly Met Lys Lys Val	
375 380 385	
gcc ggt tct ctc cgt ctg gat ctg gct gca ttc cgc gac ctg gaa gca	1315
Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe Arg Asp Leu Glu Ala	
390 395 400 405	
ttc gct acc ttc gca tct gac ttg gat gct gca tcc aag tct cag ctt	1363
Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala Ser Lys Ser Gln Leu	
410 415 420	
gag cgt ggc cag cgc ctc gtt cag ctg ttg att cag tct gag aac gca	1411
Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile Gln Ser Glu Asn Ala	
425 430 435	
cct cag gct gtt gag tac cag atc att tct ctc tgg ctt gca ggc gaa	1459
Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu Trp Leu Ala Gly Glu	
440 445 450	
ggc gca ttc gac aac gtt cct gtt gaa gat gtt cgt cgc ttc gag tcc	1507
Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val Arg Arg Phe Glu Ser	
455 460 465	

gaa ctg cac gag tac tta ggc tcc aac gct gca cag gtc tac gag cag 1555  
 Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala Gln Val Tyr Glu Gln  
 470 475 480 485  
  
 atc gct ggt gga gct cag ctt tcc gac gag tcc aag gaa acc ttg ctc 1603  
 Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser Lys Glu Thr Leu Leu  
 490 495 500  
  
 aag gca acc gaa gat ttc aag agc gct ttc cag acc acc gat ggc acc 1651  
 Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln Thr Thr Asp Gly Thr  
 505 510 515  
  
 cct gtc atc aac gag cct gag gtt gaa gca ctc gat gca ggc cag gtc 1699  
 Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu Asp Ala Gly Gln Val  
 520 525 530  
  
 aag aaa gac cag ctc acc gtt tcc cgc aag gtc agc aag aag 1741  
 Lys Lys Asp Gln Leu Thr Val Ser Arg Lys Val Ser Lys Lys  
 535 540 545  
  
 taaggcagcg agcctacact aaa 1764

<210> 760  
 <211> 547  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 760  
 Met Ala Glu Leu Thr Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala  
 1 5 10 15  
  
 Asn Tyr Thr Ser Ser Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly  
 20 25 30  
  
 Val Val Ile Ser Ala Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro  
 35 40 45  
  
 Ser Val Met Ala Asn Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly  
 50 55 60  
  
 Val Ala Gln Asn Leu Glu Ala Asp Arg Val Gly Val Val Val Leu Gly  
 65 70 75 80  
  
 Asn Tyr Glu Leu Leu Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp  
 85 90 95  
  
 Val Leu Ser Ile Pro Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn  
 100 105 110  
  
 Pro Leu Gly Gln Pro Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu  
 115 120 125  
  
 Asp Arg Val Leu Glu Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro  
 130 135 140  
  
 Val Glu Glu Pro Leu Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr  
 145 150 155 160  
  
 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr  
 165 170 175

Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn  
 180 185 190  
 Trp Glu Thr Gly Asp Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala  
 195 200 205  
 Ile Gly Gln Lys Gly Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu  
 210 215 220  
 Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser  
 225 230 235 240  
 Asp Ala Ala Gly Phe Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu  
 245 250 255  
 Ala Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp  
 260 265 270  
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu  
 275 280 285  
 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu  
 290 295 300  
 His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly  
 305 310 315 320  
 Ala Gly Ser Ile Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp  
 325 330 335  
 Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln  
 340 345 350  
 Val Phe Leu Glu Ser Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile  
 355 360 365  
 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys  
 370 375 380  
 Gly Met Lys Lys Val Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe  
 385 390 395 400  
 Arg Asp Leu Glu Ala Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala  
 405 410 415  
 Ser Lys Ser Gln Leu Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile  
 420 425 430  
 Gln Ser Glu Asn Ala Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu  
 435 440 445  
 Trp Leu Ala Gly Glu Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val  
 450 455 460  
 Arg Arg Phe Glu Ser Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala  
 465 470 475 480  
 Gln Val Tyr Glu Gln Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser  
 485 490 495

Lys Glu Thr Leu Leu Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln  
 500 505 510

Thr Thr Asp Gly Thr Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu  
 515 520 525

Asp Ala Gly Gln Val Lys Lys Asp Gln Leu Thr Val Ser Arg Lys Val  
 530 535 540

Ser Lys Lys  
 545

<210> 761  
 <211> 1572  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1549)  
 <223> RXN01193

<400> 761  
 gtgtggccaa ccaggcacgt caggcacaga tcaccagga aatcacagag attgttggtg 60

gcgcaggcgc gctcgccgac agcggagaaa gtgactaatt atg act aca gct ctt 115  
 Met Thr Thr Ala Leu  
 1 5

gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163  
 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg  
 10 15 20

gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211  
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro  
 25 30 35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259  
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys  
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307  
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile  
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355  
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala  
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403  
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val  
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451  
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser  
 105 110 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499  
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro  
 120 125 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc	547
Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly	
135 140 145	
atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc	595
Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile	
150 155 160 165	
ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa	643
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu	
170 175 180	
atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca	691
Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala	
185 190 195	
ggg gtt ggt gag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg	739
Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met	
200 205 210	
gaa gaa atg ggc gtt ctc cag gac acc gcc ctg gtg ttc ggt cag atg	787
Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu Val Phe Gly Gln Met	
215 220 225	
gat gag cca cca gga gtc ggt atg cgc gtg gct ctg tcc ggc ctg acc	835
Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala Leu Ser Gly Leu Thr	
230 235 240 245	
atg gcg gag tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc	883
Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe	
250 255 260	
atc gac aac atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc	931
Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr	
265 270 275	
ctt ctg ggt cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct	979
Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala	
280 285 290	
gac gag atg ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt	1027
Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg	
295 300 305	
tcg att acc tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc	1075
Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr	
310 315 320 325	
gac ccg gct cca gcg acc acc ttc gct cac ttg gat gca acc acc gag	1123
Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu	
330 335 340	
ctt gac cgc tcc att gct tcc aag ggt att tac cca gca gtg aac cca	1171
Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro	
345 350 355	
ctg acc tcc acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt	1219
Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg	
360 365 370	

cac tac gag gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag 1267  
 His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys  
 375 380 385

gaa ctt cag gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa 1315  
 Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu  
 390 395 400 405

gag gac aag atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg 1363  
 Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu  
 410 415 420

ggt cag aac ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc 1411  
 Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser  
 425 430 435

tac gtg cca ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac 1459  
 Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn  
 440 445 450

ggc gac ttc gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt 1507  
 Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly  
 455 460 465

ttg gac gat gtc gaa gct gca tac aag aag ctg acc gga aag 1549  
 Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys  
 470 475 480

taaggtagag acacatggct gaa 1572

<210> 762  
 <211> 483  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 762  
 Met Thr Thr Ala Leu Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala  
 1 5 10 15

Gly Arg Val Val Arg Val Ile Gly Ala Val Val Asp Val Glu Phe Pro  
 20 25 30

Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr  
 35 40 45

Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu  
 50 55 60

Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu  
 65 70 75 80

Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro  
 85 90 95

Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys  
 100 105 110

Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly  
 115 120 125



Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu  
 130 135 140  
 Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val  
 145 150 155 160  
 Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr  
 165 170 175  
 Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly  
 180 185 190  
 Thr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp  
 195 200 205  
 Leu Phe Leu Glu Met Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu  
 210 215 220  
 Val Phe Gly Gln Met Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala  
 225 230 235 240  
 Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln  
 245 250 255  
 Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly  
 260 265 270  
 Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr  
 275 280 285  
 Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr  
 290 295 300  
 Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro  
 305 310 315 320  
 Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu  
 325 330 335  
 Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr  
 340 345 350  
 Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala  
 355 360 365  
 Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile  
 370 375 380  
 Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met  
 385 390 395 400  
 Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg  
 405 410 415  
 Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr  
 420 425 430  
 Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe  
 435 440 445  
 Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe

450

455

460

Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu  
 465 470 475 480

Thr Gly Lys

<210> 763

<211> 778

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (15)..(755)

<223> FRXA01193

<400> 763

caccaggagt cggtatg cgc gtg gct ctg tcc ggc ctg acc atg gcg gag 50  
                   Met Arg Val Ala Leu Ser Gly Leu Thr Met Ala Glu  
                   1                  5                  10

tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc atc gac aac 98  
 Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn  
                   15                  20                  25

atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc ctt ctg ggt 146  
 Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly  
                   30                  35                  40

cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct gac gag atg 194  
 Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met  
                   45                  50                  55                  60

ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt tcg att acc 242  
 Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr  
                   65                  70                  75

tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc gac ccg gct 290  
 Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala  
                   80                  85                  90

cca gcg acc acc ttc gct cac ttg gat gca acc acc gag ctt gac cgc 338  
 Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg  
                   95                  100                  105

tcc att gct tcc aag ggt att tac cca gca gtg aac cca ctg acc tcc 386  
 Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser  
                   110                  115                  120

acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt cac tac gag 434  
 Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu  
                   125                  130                  135                  140

ggt tct cag cgt gtc atc ggc att ctg cag aag aac aag gaa ctt cag 482  
 Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln  
                   145                  150                  155

gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa gag gac aag 530

Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys  
 160 165 170  
 atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg ggt cag aac 578  
 Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn  
 175 180 185  
 ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc tac gtg cca 626  
 Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro  
 190 195 200  
 ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac ggc gac ttc 674  
 Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe  
 205 210 215 220  
 gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt ttg gac gat 722  
 Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp  
 225 230 235  
 gtc gaa gct gca tac aag aag ctg acc gga aag taaggtagag acacatggct 775  
 Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys  
 240 245  
 gaa 778

<210> 764  
 <211> 247  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 764  
 Met Arg Val Ala Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp  
 1 5 10 15  
 Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe  
 20 25 30  
 Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser  
 35 40 45  
 Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln  
 50 55 60  
 Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala  
 65 70 75 80  
 Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr  
 85 90 95  
 Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser  
 100 105 110  
 Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile  
 115 120 125  
 Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg  
 130 135 140  
 Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala  
 145 150 155 160

Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala  
 165 170 175

Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala  
 180 185 190

Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr  
 195 200 205

Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro  
 210 215 220

Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala  
 225 230 235 240

Tyr Lys Lys Leu Thr Gly Lys  
 245

<210> 765  
 <211> 739  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(739)  
 <223> FRXA01203

<400> 765  
 gtgtggccaa ccaggcacgt caggcacaga tcaccagga aatcacagag attgttggtg 60

gcgcaggcgc gctcgccgac agcggagaaa gtgactaatt atg act aca gct ctt 115  
 Met Thr Thr Ala Leu  
 1 5

gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163  
 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg  
 10 15 20

gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211  
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro  
 25 30 35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259  
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys  
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307  
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile  
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355  
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala  
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403  
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val  
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451  
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser  
 105 110 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499  
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro  
 120 125 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc 547  
 Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly  
 135 140 145

atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc 595  
 Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile  
 150 155 160 165

ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa 643  
 Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu  
 170 175 180

atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca 691  
 Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala  
 185 190 195

ggt gtt ggt aag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg 739  
 Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met  
 200 205 210

&lt;210&gt; 766

&lt;211&gt; 213

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 766

Met Thr Thr Ala Leu Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala  
 1 5 10 15

Gly Arg Val Val Arg Val Ile Gly Ala Val Val Asp Val Glu Phe Pro  
 20 25 30

Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr  
 35 40 45

Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu  
 50 55 60

Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu  
 65 70 75 80

Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro  
 85 90 95

Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys  
 100 105 110

Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly  
 115 120 125

Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu  
 130 135 140

Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val  
 145 150 155 160

Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr  
 165 170 175

Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly  
 180 185 190

Thr Ser Val Phe Ala Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp  
 195 200 205

Leu Phe Leu Glu Met  
 210

<210> 767  
 <211> 363  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(340)  
 <223> RXN02821

<400> 767  
 aagtcgcccc gatagcgagc ggaccactcg gtcaactgaa taacccact aaacacttca 60

cagcccgaa acacgggcac cagaaagga acgacacctc atg aac gag atc atc 115  
 Met Asn Glu Ile Ile  
 1 5

ctg gca cag gac gca acc gag tcc acc atc acc gga ctt ggc gct gtc 163  
 Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr Gly Leu Gly Ala Val  
 10 15 20

ggc tac ggc atc gca acc atc gga cct ggc ctc ggc atc ggc atc ctg 211  
 Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu  
 25 30 35

gtt ggt aag gct ctc gag ggt atg gca cgt cag cct gag atg gct gga 259  
 Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly  
 40 45 50

cag ctc cgt acc acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg 307  
 Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu  
 55 60 65

gca ctg atc ggc ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga 360  
 Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe  
 70 75 80

aag 363

<210> 768  
 <211> 80  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 768

```

Met Asn Glu Ile Ile Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr
 1             5             10             15

Gly Leu Gly Ala Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu
          20             25             30

Gly Ile Gly Ile Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln
          35             40             45

Pro Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala
          50             55             60

Phe Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
          65             70             75             80

```

&lt;210&gt; 769

&lt;211&gt; 303

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(280)

&lt;223&gt; FRXA02821

&lt;400&gt; 769

```

agcccgaaca caccgggcacc agaaagggaa cgacacctca tgaacgagat catcttggca 60

caggacgcaa ccgagtcac catcaccgga ccttggcgct gtg ggc tac ggc atc 115
                               Val Gly Tyr Gly Ile
                               1             5

gca acc atc gga cct ggc ctc ggc atc ggc atc ttg gtt ggt aag gct 163
Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu Val Gly Lys Ala
          10             15             20

ctc gag ggt atg gca cgt cag cct gag atg gct gga cag ctc cgt acc 211
Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly Gln Leu Arg Thr
          25             30             35

acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg gca ctg atc ggc 259
Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu Ala Leu Ile Gly
          40             45             50

ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga aag 303
Leu Val Ala Gly Phe Leu Phe
          55             60

```

&lt;210&gt; 770

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 770

Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile  
 1 5 10 15  
 Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala  
 20 25 30  
 Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala  
 35 40 45  
 Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe  
 50 55 60

&lt;210&gt; 771

&lt;211&gt; 632

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(609)

&lt;223&gt; RXA01200

&lt;400&gt; 771

ggc tgt ctt cgg tgg aaa agt gag cca tct gtt ctc gaa gtc ctc aag 48  
 Gly Cys Leu Arg Trp Lys Ser Glu Pro Ser Val Leu Glu Val Leu Lys  
 1 5 10 15  
 gac gcc gca gag cag acc tgg tcc act cca cgc gag ttc cgc gct gga 96  
 Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly  
 20 25 30  
 cta gtc caa ctt ggc cgt cgc gcc ctt ctt cgc tct gcg gag aaa cag 144  
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln  
 35 40 45  
 ggt cag ctt ggt cag gtg gaa gat gaa ctg ttc cga ctc agc cga atc 192  
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile  
 50 55 60  
 ctg gat cgc gaa agc aag ctg act cag ctt ctt tca gat cgc act cag 240  
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln  
 65 70 75 80  
 gaa att ggc ggt cga cgt gac ctc ctg gct aag gtg ctc tac ggc aag 288  
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys  
 85 90 95  
 gta act gct gtt acc gaa gcc ctc gca ctg cag gct att ggt cgc cct 336  
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro  
 100 105 110  
 gag cac aac cca att gac gat atc gca gct ttg gct ggc gct gta gca 384  
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala  
 115 120 125  
 gag cta cag ggt cgt tcc gtt gca cat gtc gtt acc gca gtt gaa ctc 432  
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu  
 130 135 140  
 aac gag gga cag caa caa gcg cta gct gaa aag ctg gga cgt att tat 480



Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr  
 145 150 155 160  
 ggt cgt gcg atg agc atc cac tcc gag gtt gat acc agc ctc ctc ggt 528  
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly  
 165 170 175  
 gga atg atc atc cgc gtc gga gac gaa gta att gac ggc agc acc tcg 576  
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser  
 180 185 190  
 ggc aaa ctc gag cgt ctg cgg gca agc ttc gca taaagacacg acgaattaga 629  
 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala  
 195 200  
 caa 632

<210> 772  
 <211> 203  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 772  
 Gly Cys Leu Arg Trp Lys Ser Glu Pro Ser Val Leu Glu Val Leu Lys  
 1 5 10 15  
 Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly  
 20 25 30  
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln  
 35 40 45  
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile  
 50 55 60  
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln  
 65 70 75 80  
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys  
 85 90 95  
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro  
 100 105 110  
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala  
 115 120 125  
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu  
 130 135 140  
 Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr  
 145 150 155 160  
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly  
 165 170 175  
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser  
 180 185 190  
 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala

200

```
<220>  
<221> CDS  
<222> (101)..(472)  
<223> RXA01194
```

```
<210> 774
<211> 124
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 774  
Met Ala Glu Ile Thr Val Glu Leu Val Ser Val Glu Arg Met Leu Trp  
1 5 10 15

Ala Gly Gln Ala Ser Ile Val Thr Ala Gln Thr Thr Glu Gly Glu Ile  
 20 25 30

Gly Val Leu Pro Asp His Glu Pro Leu Leu Gly Gln Leu Val Glu Asn  
 35 40 45

Gly Val Val Thr Ile Gln Pro Ile Asp Gly Glu Lys Leu Ile Ala Gly  
 50 55 60

Val Ser Asp Gly Phe Leu Ser Val Ser Lys Glu Lys Val Thr Ile Leu  
 65 70 75 80

Ala Asp Phe Ala Val Trp Ala Asn Glu Val Asp Thr Ala Ser Ala Glu  
 85 90 95

Ala Asp Leu Asn Ser Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala  
 100 105 110

Gly Leu Arg Ala Val Arg Arg Ser Ser Glu Gly Leu  
 115 120

<210> 775  
 <211> 1098  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1075)  
 <223> RXA01202

<400> 775  
 agaaagacca gctcaccgtt tcccgcaagg tcagcaagaa gtaaggcagc gagcctacac 60

taaagtactg tccaagcaac tgaagggagg cgtgtgaacc atg gca aca att cgt 115  
 Met Ala Thr Ile Arg  
 1 5

gaa ttg cgt gac cga att cgt tcg gtt aac tca acc aag aag atc acc 163  
 Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser Thr Lys Lys Ile Thr  
 10 15 20

aag gct caa gag ctc atc gcc acc tct cgc atc acc aag gca cag ggt 211  
 Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile Thr Lys Ala Gln Gly  
 25 30 35

cgc gtc gcg gca gct gcg ccg tac gcc gag gaa atc cag cgc gtg ctg 259  
 Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu Ile Gln Arg Val Leu  
 40 45 50

gag cgc ctc gcg tcg gca agc tcc cta gac cac cca atg ctg cgt gag 307  
 Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His Pro Met Leu Arg Glu  
 55 60 65

cgt gaa ggc ggc aag cga gcc gcc gtg ctc gtg gtt act tct gac cgc 355  
 Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val Val Thr Ser Asp Arg  
 70 75 80 85

ggc atg gct ggt ggc tac aac cac aac gtt ctg aaa aag gca gcg gag 403

Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu Lys Lys Ala Ala Glu	
90 95 100	
ctg gaa aag ctt ctt gct gaa agt gga tac gaa gtg gtt cgt tat gtc	451
Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu Val Val Arg Tyr Val	
105 110 115	
acc ggc aaa aag ggc gtc gac tac tac aag ttc cgc gct gaa gat gtg	499
Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe Arg Ala Glu Asp Val	
120 125 130	
gct ggc acc tgg act gga ttc tca cag gat cca gac tgg gca gct acc	547
Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro Asp Trp Ala Ala Thr	
135 140 145	
cac aac gtg cgc cgt cac ctc att gat ggt ttc acc gcc agc tct gaa	595
His Asn Val Arg Arg His Leu Ile Asp Gly Phe Thr Ala Ser Ser Glu	
150 155 160 165	
ggt gaa gct gca tgg cgc gag gga ctg aac cta cca gaa ggc cag gat	643
Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu Pro Glu Gly Gln Asp	
170 175 180	
atc cag ggc ttc gac cag gtt cac gtg gtc tac acc gag ttc atc tcc	691
Ile Gln Gly Phe Asp Gln Val His Val Val Tyr Thr Glu Phe Ile Ser	
185 190 195	
atg ctg act caa aac cca gta gtg cac caa ctg ctg cct gtt gag cca	739
Met Leu Thr Gln Asn Pro Val Val His Gln Leu Leu Pro Val Glu Pro	
200 205 210	
gtc atc gaa gat gaa att ttc gaa aaa ggc gag gat ctg ctg tcc tct	787
Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu Asp Leu Leu Ser Ser	
215 220 225	
tcc ggc gaa gtc gaa ccc gac tac gag ttc gag ccg gat gca gac act	835
Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu Pro Asp Ala Asp Thr	
230 235 240 245	
ctg ctt gag gca ctg ctt ccg cag tac gtc tct cgt agg ctg ttc tcc	883
Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser Arg Arg Leu Phe Ser	
250 255 260	
atc ttc ttg gag gct gca gct gca gag tcc gct tca cgt cga aac gcg	931
Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala Ser Arg Arg Asn Ala	
265 270 275	
atg aag tct gcg act gac aac gct acg gaa ctg gtc aag gac ctg tcc	979
Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu Val Lys Asp Leu Ser	
280 285 290	
cgt gtg gcc aac cag gca cgt cag gca cag atc acc cag gaa atc aca	1027
Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile Thr Gln Glu Ile Thr	
295 300 305	
gag att gtt ggt ggc gca ggc gcg ctc gcc gac agc gga gaa agt gac	1075
Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp Ser Gly Glu Ser Asp	
310 315 320 325	
taattatgac tacagctctt gaa	1098

&lt;210&gt; 776

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 776

Met Ala Thr Ile Arg Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser  
 1 5 10 15

Thr Lys Lys Ile Thr Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile  
 20 25 30

Thr Lys Ala Gln Gly Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu  
 35 40 45

Ile Gln Arg Val Leu Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His  
 50 55 60

Pro Met Leu Arg Glu Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val  
 65 70 75 80

Val Thr Ser Asp Arg Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu  
 85 90 95

Lys Lys Ala Ala Glu Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu  
 100 105 110

Val Val Arg Tyr Val Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe  
 115 120 125

Arg Ala Glu Asp Val Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro  
 130 135 140

Asp Trp Ala Ala Thr His Asn Val Arg Arg His Leu Ile Asp Gly Phe  
 145 150 155 160

Thr Ala Ser Ser Glu Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu  
 165 170 175

Pro Glu Gly Gln Asp Ile Gln Gly Phe Asp Gln Val His Val Val Tyr  
 180 185 190

Thr Glu Phe Ile Ser Met Leu Thr Gln Asn Pro Val Val His Gln Leu  
 195 200 205

Leu Pro Val Glu Pro Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu  
 210 215 220

Asp Leu Leu Ser Ser Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu  
 225 230 235 240

Pro Asp Ala Asp Thr Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser  
 245 250 255

Arg Arg Leu Phe Ser Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala  
 260 265 270

Ser Arg Arg Asn Ala Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu  
 275 280 285

Val Lys Asp Leu Ser Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile  
 290 295 300

Thr Gln Glu Ile Thr Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp  
 305 310 315 320

Ser Gly Glu Ser Asp  
 325

&lt;210&gt; 777

&lt;211&gt; 1773

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1750)

&lt;223&gt; RXN02434

&lt;400&gt; 777

cttcaatagt caaaaccagc aaactaat ttttaagtttt acgtaactgg cccacccgct 60

tgtggcaggc cttgcgtttt gacattgaag gacccttttt atg cgc act ttt gcc 115  
 Met Arg Thr Phe Ala  
 1 5

gct tat att gcc att gat ggc ctc agc ttt tcc tac ccc aac acc cac 163  
 Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His  
 10 15 20

gtt tta agc gat att tcg ctc acc gtt gcc aat ggc gat atc gcc gga 211  
 Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn Gly Asp Ile Ala Gly  
 25 30 35

ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc agc ctc atc 259  
 Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile  
 40 45 50

gct ggc gtc atg gaa ccc gac cag ggc agg att tac ctc ccc gaa cgc 307  
 Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile Tyr Leu Pro Glu Arg  
 55 60 65

acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg 355  
 Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val  
 70 75 80 85

cag tcg ctt atc gac gcc gcc gtc gcc cca gtg cgc gcg gtc gat gcc 403  
 Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val Arg Ala Val Asp Ala  
 90 95 100

gcg att aca gat ttg tcc acc aag ctt ggc gac gcc tcc ctc agc gcc 451  
 Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp Ala Ser Leu Ser Ala  
 105 110 115

gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta gcc gct 499  
 Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala  
 120 125 130

gca gaa gaa ctc gga ctg tgg gaa tta gat gca cgt att gaa acc atc 547  
 Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala Arg Ile Glu Thr Ile

135	140	145	
gtc gcg ggt ctc ggc ctt gcc gag gtg gat cgc agc act ccc att ggt Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg Ser Thr Pro Ile Gly 150 155 160 165			595
gag ctt tcc ggc ggt cag cgc cgc aga ttc gca ttg gca gcg ctg ctg Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala Leu Ala Ala Leu Leu 170 175 180			643
ttg gaa cca cac gat gct ctg att ttc gat gag ccc acc aac cac ctc Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu Pro Thr Asn His Leu 185 190 195			691
gac gac aca gcc gta gat ttc ctc atc tcg gag att tcc cgt ttc aaa Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu Ile Ser Arg Phe Lys 200 205 210			739
ggt cca gtg ctg atc gcc agc cac gat cgc ttc ttc ctc gac tcc gtc Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe Phe Leu Asp Ser Val 215 220 225			787
tgt acc gag tta atc gac ctc gat cct gca ctt gga cct gag ggc gga Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu Gly Pro Glu Gly Gly 230 235 240 245			835
tcc ggc gaa gaa gta aaa caa gcc gtg tct ttt ggt ggt gga ttt tct Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe Gly Gly Gly Phe Ser 250 255 260			883
gaa tac atc aaa gaa cgc gag acc cgc cgc acc cgc tgg gct cag ttg Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr Arg Trp Ala Gln Leu 265 270 275			931
tac acc gca caa gaa acc gag cgg gaa aaa ctc gaa gaa acc acc ggc Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu Glu Glu Thr Thr Gly 280 285 290			979
acc acc gaa tcg gat att ttc cac agc tcg gtt tcc aaa tcg gaa gct Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val Ser Lys Ser Glu Ala 295 300 305			1027
aaa atc acc gcg aaa ttt tac gca gac cgg gca gct aaa act caa ggc Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala Ala Lys Thr Gln Gly 310 315 320 325			1075
aac cgc gtc cgc tcc gcc aaa aac cgc ctg aag gaa ttg gaa cgc tat Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys Glu Leu Glu Arg Tyr 330 335 340			1123
gaa atc cca gca cct cca aag cca ctg gaa ttc caa ggc atc cca gaa Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe Gln Gly Ile Pro Glu 345 350 355			1171
gcc tcc gga aac ggt cac ggt gaa aca cta gaa gtg cgg gct att gct Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu Val Arg Ala Ile Ala 360 365 370			1219
gtg gaa aac agg ctt caa ccc ttg act ttc cac atc gat ccc ggc gac Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His Ile Asp Pro Gly Asp 375 380 385			1267

cac atc ctg gtc gaa ggc ccc aac ggt gtc ggt aaa tcc acc ctg ctg 1315  
 His Ile Leu Val Glu Gly Pro Asn Gly Val Gly Lys Ser Thr Leu Leu  
 390 395 400 405  
 agc gtt ctg gaa ggc gtg ctt gaa cca acc gaa ggt gaa ttg atc gtc 1363  
 Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu Gly Glu Leu Ile Val  
 410 415 420  
 ccc gaa ggg ctg aaa gtt gcg cgc ctg aaa cag gac gat cag tgg acg 1411  
 Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln Asp Asp Gln Trp Thr  
 425 430 435  
 gaa aag cag ttg aac acc ccc gtc gac gaa ctg ttc gcc gcc cta tcg 1459  
 Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu Phe Ala Ala Leu Ser  
 440 445 450  
 aaa ggt ccg gtc gga ctc aac ctc gtg gag atg ggg ctg ttg agg gag 1507  
 Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met Gly Leu Leu Arg Glu  
 455 460 465  
 acg tcg caa agc agc ccg cta cgg gcc cta tcg ctc ggc caa cgc cgg 1555  
 Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser Leu Gly Gln Arg Arg  
 470 475 480 485  
 cgc gtc tcg ctc ggg ctc atc ctg gcg agc cca cca gat ctt ttg ctt 1603  
 Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro Pro Asp Leu Leu Leu  
 490 495 500  
 ctt gac gag ccc acc aac cac ctc tcc ctc gcg ctg agc gaa gaa ctc 1651  
 Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala Leu Ser Glu Glu Leu  
 505 510 515  
 gag tcg gcg ata gaa aaa ttc ccc ggt cgc gtt att ctg gcc agc cac 1699  
 Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val Ile Leu Ala Ser His  
 520 525 530  
 gat agg tgg atc aga aaa cgt tgg acg ggg aag aaa atc agc ctg agc 1747  
 Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys Lys Ile Ser Leu Ser  
 535 540 545  
 cgt taaaccctac tgaacaggaa cct 1773  
 Arg  
 550

&lt;210&gt; 778

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 778

Met Arg Thr Phe Ala Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser  
 1 5 10 15  
 Tyr Pro Asn Thr His Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn  
 20 25 30  
 Gly Asp Ile Ala Gly Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr  
 35 40 45



Leu Leu Ser Leu Ile Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile  
 50 55 60  
 Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro  
 65 70 75 80  
 Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val  
 85 90 95  
 Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp  
 100 105 110  
 Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp  
 115 120 125  
 Ala Ala Leu Gly Ala Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala  
 130 135 140  
 Arg Ile Glu Thr Ile Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg  
 145 150 155 160  
 Ser Thr Pro Ile Gly Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala  
 165 170 175  
 Leu Ala Ala Leu Leu Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu  
 180 185 190  
 Pro Thr Asn His Leu Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu  
 195 200 205  
 Ile Ser Arg Phe Lys Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe  
 210 215 220  
 Phe Leu Asp Ser Val Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu  
 225 230 235 240  
 Gly Pro Glu Gly Gly Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe  
 245 250 255  
 Gly Gly Gly Phe Ser Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr  
 260 265 270  
 Arg Trp Ala Gln Leu Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu  
 275 280 285  
 Glu Glu Thr Thr Gly Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val  
 290 295 300  
 Ser Lys Ser Glu Ala Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala  
 305 310 315 320  
 Ala Lys Thr Gln Gly Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys  
 325 330 335  
 Glu Leu Glu Arg Tyr Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe  
 340 345 350  
 Gln Gly Ile Pro Glu Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu  
 355 360 365  
 Val Arg Ala Ile Ala Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His

370 375 380  
 Ile Asp Pro Gly Asp His Ile Leu Val Glu Gly Pro Asn Gly Val Gly  
 385 390 395 400  
 Lys Ser Thr Leu Leu Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu  
 405 410 415  
 Gly Glu Leu Ile Val Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln  
 420 425 430  
 Asp Asp Gln Trp Thr Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu  
 435 440 445  
 Phe Ala Ala Leu Ser Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met  
 450 455 460  
 Gly Leu Leu Arg Glu Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser  
 465 470 475 480  
 Leu Gly Gln Arg Arg Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro  
 485 490 495  
 Pro Asp Leu Leu Leu Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala  
 500 505 510  
 Leu Ser Glu Glu Leu Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val  
 515 520 525  
 Ile Leu Ala Ser His Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys  
 530 535 540  
 Lys Ile Ser Leu Ser Arg  
 545 550  
  
 <210> 779  
 <211> 1407  
 <212> DNA  
 <213> *Corynebacterium glutamicum*  
  
 <220>  
 <221> CDS  
 <222> (101)..(1384)  
 <223> RXN00684  
  
 <400> 779  
 agtcacacct aaaagtgata gccatcacga atctttagga aaagtgattc aaacttcact 60  
  
 gtgatcggct tcggccacac acaagtgtca ggagatgaca atg act tcc cag act 115  
 Met Thr Ser Gln Thr  
 1 5  
  
 tcc caa caa tcc acc tca acc ggt gga tgc cca ttc ggg cac aca tca 163  
 Ser Gln Gln Ser Thr Ser Thr Gly Gly Cys Pro Phe Gly His Thr Ser  
 10 15 20  
  
 gag tcc acc agc cat cac ggc tac cag cct ttc gat atg cac aac ccg 211  
 Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe Asp Met His Asn Pro  
 25 30 35

ttt cct gca tat aaa gaa ctc cgt cag gaa gag cca gtg atg ttc gat	259
Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu Pro Val Met Phe Asp	
40 45 50	
gag cgc atc ggc tac tgg gtg gta acc aaa tat gac gac atc aaa acc	307
Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr Asp Asp Ile Lys Thr	
55 60 65	
acc ttt gat gac tgg gaa aca ttc tcc tct gaa aat gca caa gcc cca	355
Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu Asn Ala Gln Ala Pro	
70 75 80 85	
gtc cgc aag cgt gga cct cag gca acc caa atc atg acc gat ggc ggc	403
Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile Met Thr Asp Gly Gly	
90 95 100	
ttc act gca tac tcc gga tta tca gct cgt att cca cca gag cac acc	451
Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile Pro Pro Glu His Thr	
105 110 115	
cgc atc cgc gca atc gca caa aag gcc ttc acg cca cgc cgc tat aaa	499
Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr Pro Arg Arg Tyr Lys	
120 125 130	
gca ctc gaa cca gat atc cga gca atg gtg att gat cgt gtg gag aaa	547
Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile Asp Arg Val Glu Lys	
135 140 145	
atg ttg gcg aat gat caa cac gtc ggc gat atg gtg tca gat ctt gcc	595
Met Leu Ala Asn Asp Gln His Val Gly Asp Met Val Ser Asp Leu Ala	
150 155 160 165	
tac gac att cca acc atc acg atc ctg acg ctg atc ggt gca gat att	643
Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu Ile Gly Ala Asp Ile	
170 175 180	
ttc atg gtg gtc acc tac aag cgg tgg tca gat tcc cgt gcg gcc atg	691
Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp Ser Arg Ala Ala Met	
185 190 195	
acc tgg ggc gat ctt agt gat gaa gag cag atc cca cac gca cac aat	739
Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile Pro His Ala His Asn	
200 205 210	
ttg gtt gag tac tgg cag gaa tgc caa cgc atg gta gct gat gca cat	787
Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met Val Ala Asp Ala His	
215 220 225	
gca cac ggt ggc gac aac ctc acc gct gat cta gtg cga gca cag caa	835
Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu Val Arg Ala Gln Gln	
230 235 240 245	
gag ggt caa gaa atc acc gat cat gag att gct tct ttg ctg tac tcc	883
Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala Ser Leu Leu Tyr Ser	
250 255 260	
ctg ctt ttt gcg ggg cac gaa aca acc acc acg ttg atc tcc aat tgt	931
Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr Leu Ile Ser Asn Cys	
265 270 275	
ttc cga gtt ctc ctc gat cat cca gag cag tgg caa gcc att cta gag	979

Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp Gln Ala Ile Leu Glu  
 280 285 290  
 aat cca aaa ctg att cct gcg gca gtg gat gag gtc ttg cgg tac tcc 1027  
 Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu Val Leu Arg Tyr Ser  
 295 300 305  
 ggc tcg atc gtg ggg tgg cgt cga aaa gca tta aaa gac acc gag atc 1075  
 Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu Lys Asp Thr Glu Ile  
 310 315 320 325  
 ggc ggc gtt gcc att aag gaa ggc gat ggt gtt ctg ctg ctc atg ggt 1123  
 Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val Leu Leu Leu Met Gly  
 330 335 340  
 tcc gcg aac cgc gat gaa gct cgc ttt gaa aat ggc gag gaa ttc gat 1171  
 Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn Gly Glu Glu Phe Asp  
 345 350 355  
 atc agc cgc gct aat gcg cgc gag cac ctg tct ttt ggt ttc ggc atc 1219  
 Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser Phe Gly Phe Gly Ile  
 360 365 370  
 cac tat tgc cta gga aac atg ctg gcc aaa ctt caa gcc aag atc tgt 1267  
 His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu Gln Ala Lys Ile Cys  
 375 380 385  
 ctc gag gaa gtc acc agg ctt gtt cct tcc ctg cac ttg gtt gcg gac 1315  
 Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu His Leu Val Ala Asp  
 390 395 400 405  
 aaa gct atc ggg ttc cgg gag aac ctc tcc ttc cgc gtc ccc act tct 1363  
 Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe Arg Val Pro Thr Ser  
 410 415 420  
 gtt ccc gtg act tgg aac gct taacgcttta ttaaataagg aga 1407  
 Val Pro Val Thr Trp Asn Ala  
 425

&lt;210&gt; 780

&lt;211&gt; 428

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 780

Met Thr Ser Gln Thr Ser Gln Gln Ser Thr Ser Thr Gly Gly Cys Pro  
 1 5 10 15  
 Phe Gly His Thr Ser Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe  
 20 25 30  
 Asp Met His Asn Pro Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu  
 35 40 45  
 Pro Val Met Phe Asp Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr  
 50 55 60  
 Asp Asp Ile Lys Thr Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu  
 65 70 75 80

Asn Ala Gln Ala Pro Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile  
 85 90 95  
 Met Thr Asp Gly Gly Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile  
 100 105 110  
 Pro Pro Glu His Thr Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr  
 115 120 125  
 Pro Arg Arg Tyr Lys Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile  
 130 135 140  
 Asp Arg Val Glu Lys Met Leu Ala Asn Asp Gln His Val Gly Asp Met  
 145 150 155 160  
 Val Ser Asp Leu Ala Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu  
 165 170 175  
 Ile Gly Ala Asp Ile Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp  
 180 185 190  
 Ser Arg Ala Ala Met Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile  
 195 200 205  
 Pro His Ala His Asn Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met  
 210 215 220  
 Val Ala Asp Ala His Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu  
 225 230 235 240  
 Val Arg Ala Gln Gln Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala  
 245 250 255  
 Ser Leu Leu Tyr Ser Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr  
 260 265 270  
 Leu Ile Ser Asn Cys Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp  
 275 280 285  
 Gln Ala Ile Leu Glu Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu  
 290 295 300  
 Val Leu Arg Tyr Ser Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu  
 305 310 315 320  
 Lys Asp Thr Glu Ile Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val  
 325 330 335  
 Leu Leu Leu Met Gly Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn  
 340 345 350  
 Gly Glu Glu Phe Asp Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser  
 355 360 365  
 Phe Gly Phe Gly Ile His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu  
 370 375 380  
 Gln Ala Lys Ile Cys Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu  
 385 390 395 400  
 His Leu Val Ala Asp Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe

405

410

415

Arg Val Pro Thr Ser Val Pro Val Thr Trp Asn Ala  
420 425

&lt;210&gt; 781

&lt;211&gt; 978

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(955)

&lt;223&gt; RXN00387

&lt;400&gt; 781

ttccgcgcgcg ggcgcaactt cgacggcacc gggctgacca ccttctgctt tgaagcgac 60

gatttctccg ccgactacct cgccaacggg ccaggccgag atg ttc cgc tcg aat 115  
Met Phe Arg Ser Asn  
1 5

att tcc tac gca gtc ggc gac gac atc caa aac gac cca gaa acc tgg 163  
Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn Asp Pro Glu Thr Trp  
10 15 20

gaa gac tac gaa ctt cgc gtc aac cac cca ctg cgc atc gaa ggc gac 211  
Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu Arg Ile Glu Gly Asp  
25 30 35

cgc gtc tac ctt cag ggc cac ggc ttc gcc cca aca ttc acc gtg acc 259  
Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro Thr Phe Thr Val Thr  
40 45 50

tgg cca aat ggc gag acc cgc acc cag acc gtg cag tgg cgc cca gac 307  
Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val Gln Trp Arg Pro Asp  
55 60 65

gac ccg acc ttc ttc ctg tcc tca ggc gtg gtc cgt ttc gat cca ccc 355  
Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val Arg Phe Asp Pro Pro  
70 75 80 85

gcc ggc atg tac cca gac ctt tac gag cgc cgc caa aac cag ttg gcc 403  
Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg Gln Asn Gln Leu Ala  
90 95 100

atc cag gga ctt ttc gca ccg acc gcg gaa tgg gaa ggc gac aac aac 451  
Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp Glu Gly Asp Asn Asn  
105 110 115

gaa ctg ctg acc tcc tcc tac ccg gcg atg cgt gac cca gcc gtg gcg 499  
Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg Asp Pro Ala Val Ala  
120 125 130

atc gat att tac cgc ggc gac aat ggc ctc gat acc ggc atc gga cag 547  
Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp Thr Gly Ile Gly Gln  
135 140 145

tca ttg ttc agc ctg gac tct agt ctc atg cac agc ggc gtg ctg caa 595  
Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His Ser Gly Val Leu Gln

150	155	160	165	
aaa att gag cgc gtc aac ctc caa atc ggc gac acc gtc acc ctg gat				643
Lys Ile Glu Arg Val Asn Leu Gln Ile Gly Asp Thr Val Thr Leu Asp				
	170	175	180	
gat ggc acc acc gtc tcc ttc gac ggc gcg tca gaa ttt gcc aac tac				691
Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser Glu Phe Ala Asn Tyr				
	185	190	195	
cag atc agc cgc gac ccc aca caa aac tgg gtg ctg gtc acc acc gtg				739
Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val Leu Val Thr Thr Val				
	200	205	210	
att tcg ctg gtc tcc ctg gtt gga tcc ctg atg atc cga cgc cgc cgc				787
Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met Ile Arg Arg Arg Arg				
	215	220	225	
att tgg gtg cgt ttc tat cca caa gaa aac gga acc acc cgc gtg gaa				835
Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly Thr Thr Arg Val Glu				
	230	235	240	245
acc ggc gga ctt gcc cgc acc gac cgc gca ggc tgg ggt ggc gaa tac				883
Thr Gly Gly Leu Ala Arg Thr Asp Arg Ala Gly Trp Gly Gly Glu Tyr				
	250	255	260	
gag aaa ttc cac cgc gaa ctg ctg ggt ctg aag gag gaa gat gaa gac				931
Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys Glu Glu Asp Glu Asp				
	265	270	275	
gaa gag tac ttc gac cac gac gac taacaccgca atttaaaggc ttt				978
Glu Glu Tyr Phe Asp His Asp Asp				
	280	285		

&lt;210&gt; 782

&lt;211&gt; 285

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 782

Met Phe Arg Ser Asn Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn	
1 5 10 15	

Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu	
20 25 30	

Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro	
35 40 45	

Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val	
50 55 60	

Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val	
65 70 75 80	

Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg	
85 90 95	

Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp	
100 105 110	

Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg  
 115 120 125  
 Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp  
 130 135 140  
 Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His  
 145 150 155 160  
 Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile Gly Asp  
 165 170 175  
 Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser  
 180 185 190  
 Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val  
 195 200 205  
 Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met  
 210 215 220  
 Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly  
 225 230 235 240  
 Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg Ala Gly  
 245 250 255  
 Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys  
 260 265 270  
 Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp  
 275 280 285

BGI-126CPPC - 6 -

BGI-126CPPC - 19 -